

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 5, 2006, 11:22:48 ; Search time 138.109 Seconds
 (without alignments)
 2059.155 Million cell updates/sec

Title: US-10-506-624-2
 Perfect score: 3257
 Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 622

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	3257	100.0	622	8	ADJ65161 Potassium
2	3130.5	96.1	603	5	AAE22088 Human nov
3	3130.5	96.1	603	8	ADJ65163 Potassium
4	1867.5	57.3	644	7	ADE31661 Human 692
5	1867.5	57.3	704	9	ADX38838 Human can
6	1867.5	57.3	709	9	ADX38836 Human can
7	1852	56.9	480	4	ABG12623 Novel hum

8	1845	56.6	593	9	ADX38840	Adx38840	Human	can
9	1826.5	56.1	353	5	AAE22090	Aae22090	Human	nov
10	1823	56.0	630	5	ABP69673	Abp69673	Human	pol
11	1683.5	51.7	352	7	ADM04873	Adm04873	Human	pro
12	1683.5	51.7	352	9	AEC87803	Aec87803	Human	cDN
13	1657	50.9	316	5	AAE22089	Aae22089	Human	nov
14	1051.5	32.3	661	5	ABB84485	Abb84485	Human	NCK
15	1051.5	32.3	661	6	AAO29752	Aao29752	Human	577
16	1051.5	32.3	661	7	ADE54756	Ade54756	Human	Pro
17	1051.5	32.3	661	8	ADH51637	Adh51637	Human	NCK
18	1049.5	32.2	618	4	AAM78712	Aam78712	Human	pro
19	1033	31.7	670	7	ADE54754	Ade54754	Rat	Prote
20	998	30.6	856	4	ABB60425	Abb60425	Drosophil	
21	986	30.3	658	4	ABB57820	Abb57820	Drosophil	
22	984	30.2	459	9	ADX38839	Adx38839	Human	can
23	954	29.3	500	7	ADF69521	Adf69521	Novel	hum
24	944.5	29.0	1081	7	ADJ68492	Adj68492	Human	hea
25	932.5	28.6	591	8	ADN23810	Adn23810	Bacterial	
26	932.5	28.6	591	8	ADN23811	Adn23811	Bacterial	
27	907.5	27.9	235	3	AAB25742	Aab25742	Human	sec
28	866.5	26.6	611	8	ADN22551	Adn22551	Bacterial	
29	837	25.7	169	3	AAB25701	Aab25701	Human	sec
30	837	25.7	169	6	ADA57589	Ada57589	Human	sec
31	837	25.7	169	6	ADA41486	Ada41486	Human	sec
32	837	25.7	169	6	ABR48142	Abr48142	Human	sec
33	837	25.7	169	6	ABR00299	Abr00299	Human	gen
34	837	25.7	169	7	ADB91829	Adb91829	Human	sec
35	837	25.7	169	7	ADC74600	Adc74600	Human	sec
36	773	23.7	481	4	ABB58790	Abb58790	Drosophil	
37	723	22.2	137	4	ABG12622	Abg12622	Novel	hum
38	703.5	21.6	168	3	AAB25680	Aab25680	Human	sec
39	703.5	21.6	168	6	ADA57284	Ada57284	Human	sec
40	703.5	21.6	168	6	ADA41165	Ada41165	Human	sec
41	703.5	21.6	168	6	ABR47960	Abr47960	Human	sec
42	703.5	21.6	168	6	ABR00186	Abr00186	Human	gen
43	703.5	21.6	168	7	ADB91690	Adb91690	Human	sec
44	703.5	21.6	168	7	ADC74369	Adc74369	Human	sec
45	693	21.3	168	2	AAAY45263	Aay45263	Human	sec

Search completed: August 5, 2006, 11:27:48
 Job time : 139.109 secs

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OM protein - protein search, using sw model

Run on: August 5, 2006, 11:23:23 ; Search time 195.486 Seconds
(without alignments)
2943.231 Million cell updates/sec

Title: US-10-506-624-2
Perfect score: 3257
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMSREDD 622

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3174	97.5	605	1 NCKX4_HUMAN	Q8nff2 homo sapien
2	3035	93.2	605	1 NCKX4_MOUSE	Q8cgg8 mus musculu
3	1979.5	60.8	569	2 Q567G1_BRARE	Q567g1 brachydanio
4	1902.5	58.4	504	2 Q4RA60_TETNG	Q4ra60 tetraodon n
5	1867.5	57.3	644	2 Q9H417_HUMAN	Q9h417 homo sapien
6	1866.5	57.3	644	1 NCKX3_HUMAN	Q9hc58 homo sapien
7	1860	57.1	645	1 NCKX3_MOUSE	Q99pd7 mus musculu
8	1842.5	56.6	624	1 NCKX3_RAT	Q9epq0 rattus norv
9	1838.5	56.4	595	2 Q8VD29_MOUSE	Q8vd29 mus musculu
10	1691.5	51.9	569	2 Q4S2I3_TETNG	Q4s2i3 tetraodon n
11	1640	50.4	588	2 Q4RZL6_TETNG	Q4rzl6 tetraodon n
12	1291	39.6	529	2 Q4SFH8_TETNG	Q4sfh8 tetraodon n
13	1183	36.3	557	2 Q4RPD9_TETNG	Q4rpd9 tetraodon n
14	1091.5	33.5	536	2 Q5TVP5_ANOGA	Q5tvp5 anopheles g
15	1088	33.4	538	2 Q7QH05_ANOGA	Q7qh05 anopheles g

16	1051.5	32.3	661	1	NCKX2_HUMAN	Q9ui40	homo sapien
17	1039.5	31.9	666	2	Q8BUN9_MOUSE	Q8bun9	mus musculu
18	1033	31.7	670	1	NCKX2_RAT	O54701	rattus norv
19	1030.5	31.6	651	1	NCKX2_CHICK	Q9ial7	gallus gall
20	1029.5	31.6	628	2	Q7PQ73_ANOGA	Q7pq73	anopheles g
21	1023.5	31.4	576	2	Q7PNG2_ANOGA	Q7png2	anopheles g
22	1016	31.2	526	2	Q7PLW1_DROME	Q7plw1	drosophila
23	1016	31.2	535	2	Q8SXS9_DROME	Q8sxs9	drosophila
24	1016	31.2	542	2	Q5LJX8_DROME	Q5ljx8	drosophila
25	1013	31.1	663	1	NCKX1_CHICK	Q9ial8	gallus gall
26	1012	31.1	547	2	Q5TQC5_ANOGA	Q5tqc5	anopheles g
27	1004	30.8	642	2	Q8IPM4_DROME	Q8ipm4	drosophila
28	1000.5	30.7	1043	2	Q4RGI0_TETNG	Q4rgi0	tetraodon n
29	998	30.6	856	1	NCKX_DROME	Q9u6a0	drosophila
30	998	30.6	888	2	Q8IPE3_DROME	Q8ipe3	drosophila
31	980	30.1	1014	2	O62805_TURTR	O62805	tursiops tr
32	977	30.0	513	1	NCKX5_BRARE	Q49sh1	brachydanio
33	965	29.6	596	2	Q7PSK6_ANOGA	Q7psk6	anopheles g
34	954	29.3	500	1	NCKX5_HUMAN	Q7lrs6	homo sapien
35	950.5	29.2	585	2	Q61JX9_CAEBR	Q61jx9	caenorhabdi
36	944.5	29.0	1099	1	NCKX1_HUMAN	O60721	homo sapien
37	932.5	28.6	591	2	O62088_CAEEL	O62088	caenorhabdi
38	925.5	28.4	487	2	Q4SHN8_TETNG	Q4shn8	tetraodon n
39	921.5	28.3	647	2	Q4SLY4_TETNG	Q4sly4	tetraodon n
40	921.5	28.3	1130	2	Q91WD8_MOUSE	Q91wd8	mus musculu
41	915.5	28.1	501	1	NCKX5_MOUSE	Q8c261	mus musculu
42	915	28.1	1216	1	NCKX1_BOVIN	Q28139	bos taurus
43	893	27.4	1181	1	NCKX1_RAT	Q9qzm6	rattus norv
44	884	27.1	596	2	Q61XS1_CAEBR	Q61xs1	caenorhabdi
45	872.5	26.8	596	2	O62306_CAEEL	O62306	caenorhabdi

Search completed: August 5, 2006, 11:34:20

Job time : 197.486 secs

ALIGNMENTS

RESULT 1

NCKX4_HUMAN

ID NCKX4_HUMAN STANDARD; PRT; 605 AA.
 AC Q8NFF2; Q8N8U6; Q8NCX1; Q8NFF0; Q8NFF1;
 DT 26-SEP-2003, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 32.
 DE Sodium/potassium/calcium exchanger 4 precursor (Na(+)/K(+)/Ca(2+) -
 DE exchange protein 4).
 GN Name=SLC24A4; Synonyms=NCKX4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=22359087; PubMed=12379639; DOI=10.1074/jbc.M210011200;
 RA Li X.-F., Kraev A.S., Lytton J.;
 RT "Molecular cloning of a fourth member of the potassium-dependent
 RT sodium-calcium exchanger gene family, NCKX4."
 RL J. Biol. Chem. 277:48410-48417(2002). *December*
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 4).
 RX PubMed=14702039; DOI=10.1038/ngl285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;

RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 277-605.
RC TISSUE=Testis;
RG The German cDNA consortium;
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Transports 1 Ca(2+) and 1 K(+) in exchange for 4 Na(+).
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=Q8NFF2-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8NFF2-2; Sequence=VSP_008369;
CC Name=3;
CC IsoId=Q8NFF2-3; Sequence=VSP_008372;
CC Name=4;
CC IsoId=Q8NFF2-4; Sequence=VSP_008370, VSP_008371, VSP_008373,
CC VSP_008374;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Expressed abundantly in all regions of the
CC brain, aorta, lung and thymus. Expressed at lower levels in the
CC stomach and intestine.
CC -!- SIMILARITY: Belongs to the sodium/potassium/calcium exchanger
CC family. SLC24A subfamily.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF520704; AAM76070.1; -; mRNA.
DR EMBL; AF520705; AAM76071.1; -; mRNA.
DR EMBL; AF520706; AAM76072.1; -; mRNA.

DR EMBL; AK096171; BAC04715.1; -; mRNA.
 DR EMBL; BC069653; AAH69653.1; -; mRNA.
 DR EMBL; AL834225; CAD38903.1; ALT_INIT; mRNA.
 DR Ensembl; ENSG00000140090; Homo sapiens.
 DR HGNC; HGNC:10978; SLC24A4.
 DR InterPro; IPR004481; K_NaCaexchnng.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR PANTHER; PTHR10846; K_NaCaexchnng; 1.
 DR Pfam; PF01699; Na_Ca_ex; 2.
 DR TIGRFAMs; TIGR00367; K_NaCaexchnng; 1.
 KW Alternative splicing; Antiport; Calcium; Calcium transport;
 KW Glycoprotein; Ion transport; Membrane; Potassium; Potassium transport;
 KW Repeat; Signal; Sodium; Sodium transport; Symport; Transmembrane;
 KW Transport.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 605 Sodium/potassium/calcium exchanger 4.
 FT /FTId=PRO_0000019373.
 FT TOPO_DOM 22 80 Extracellular (Potential).
 FT TRANSMEM 81 101 Potential.
 FT TOPO_DOM 102 155 Cytoplasmic (Potential).
 FT TRANSMEM 156 176 Potential.
 FT TOPO_DOM 177 183 Extracellular (Potential).
 FT TRANSMEM 184 204 Potential.
 FT TOPO_DOM 205 207 Cytoplasmic (Potential).
 FT TRANSMEM 208 228 Potential.
 FT TOPO_DOM 229 407 Extracellular (Potential).
 FT TRANSMEM 408 428 Potential.
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 FT TRANSMEM 441 461 Potential.
 FT TOPO_DOM 462 462 Extracellular (Potential).
 FT TRANSMEM 463 483 Potential.
 FT TOPO_DOM 484 509 Cytoplasmic (Potential).
 FT TRANSMEM 510 530 Potential.
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 FT TRANSMEM 541 561 Potential.
 FT TOPO_DOM 562 569 Cytoplasmic (Potential).
 FT TRANSMEM 570 590 Potential.
 FT TOPO_DOM 591 605 Extracellular (Potential).
 FT REPEAT 122 162 Alpha-1.
 FT REPEAT 478 509 Alpha-2.
 FT COMPBIAS 378 389 Poly-Pro.
 FT CARBOHYD 52 52 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 59 59 N-linked (GlcNAc . . .) (Potential).
 FT VARSPLIC 1 92 Missing (in isoform 4).
 FT /FTId=VSP_008370.
 FT VARSPLIC 1 47 Missing (in isoform 2).
 FT /FTId=VSP_008369.
 FT VARSPLIC 155 193 Missing (in isoform 4).
 FT /FTId=VSP_008371.
 FT VARSPLIC 258 276 Missing (in isoform 3).
 FT /FTId=VSP_008372.
 FT VARSPLIC 458 483 VTIIGYTLGIPDVIMGITFLAAGTSV -> EQREGKQFQHG
 FT CSSVDCETHSQPLTP (in isoform 4).
 FT /FTId=VSP_008373.
 FT VARSPLIC 484 605 Missing (in isoform 4).
 FT /FTId=VSP_008374.
 FT CONFLICT 427 427 C -> S (in Ref. 2).

SQ SEQUENCE 605 AA; 66951 MW; E032612F61FA8E1A CRC64;

Query Match 97.5%; Score 3174; DB 1; Length 605;

Best Local Similarity 100.0%; Pred. No. 1.8e-217;

Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      18 MLPQQVGFVCAVLALVCCASGLFGSLGHKTASASKRVLPDTRNRKLMAVNGTQTAKNC 77
      |||
Db      1 MLPQQVGFVCAVLALVCCASGLFGSLGHKTASASKRVLPDTRNRKLMAVNGTQTAKNC 60

Qy     78 TDPAIHEFPTDLFSNKERQHGA VLLHLGALYMFYALAIVCDDFFVPSLEKICERLHLSE 137
      |||
Db     61 TDPAIHEFPTDLFSNKERQHGA VLLHLGALYMFYALAIVCDDFFVPSLEKICERLHLSE 120

Qy    138 DVAGATFMAAGSSTPELFA SVIGVFITHGDVGVGTIVGSAVFNILCIIGVCGLFAGQVVR 197
      |||
Db    121 DVAGATFMAAGSSTPELFA SVIGVFITHGDVGVGTIVGSAVFNILCIIGVCGLFAGQVVR 180

Qy    198 LTWWAVCRDSVYYTISVIVLIVFIYDEQIVWWEGLVLIILYVFYILIMKYNVKMQAFFTV 257
      |||
Db    181 LTWWAVCRDSVYYTISVIVLIVFIYDEQIVWWEGLVLIILYVFYILIMKYNVKMQAFFTV 240

Qy    258 KQKSIANGNPVNSELEAGNDFYDGSYDDPSVPLLGVKEKPQYGKNPVVMDEIMSSSP 317
      |||
Db    241 KQKSIANGNPVNSELEAGNDFYDGSYDDPSVPLLGVKEKPQYGKNPVVMDEIMSSSP 300

Qy    318 KFTFPEAGLRIMITNKFGRTRLRMASRIIINERQRLINSANGVSSKPLQNGRHENIENG 377
      |||
Db    301 KFTFPEAGLRIMITNKFGRTRLRMASRIIINERQRLINSANGVSSKPLQNGRHENIENG 360

Qy    378 NVPVENPEDPQQNQEQPPPQPPPEPEPEVEADFLSPFSVPEAR GDKVKWVFTWPLIFLL 437
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Db    361 NVPVENPEDPQQNQEQPPPQPPPEPEPEVEADFLSPFSVPEAR GDKVKWVFTWPLIFLL 420

Qy    438 CVTIPNCSKPRWEKFFMVTFITATLWIAVFSYIMVWLVTIIGYTLGIPDVIMGITFLAAG 497
      |||
Db    421 CVTIPNCSKPRWEKFFMVTFITATLWIAVFSYIMVWLVTIIGYTLGIPDVIMGITFLAAG 480

Qy    498 TSVPDCLMASLIVARQGLGDMAVSNTIGSNVFDILVGLGVPWGLQTMVVNYGSTVKINSRG 557
      |||
Db    481 TSVPDCLMASLIVARQGLGDMAVSNTIGSNVFDILVGLGVPWGLQTMVVNYGSTVKINSRG 540

Qy    558 LVYSVLLLG SVALTVLGIHLNKR LDRKLG VYVLVLYAIFLCFSIMIEFNVFTFVNLP 617
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Qy    618 CREDD 622
      ||||
Db    601 CREDD 605
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 5, 2006, 11:34:38 ; Search time 36.5584 Seconds
(without alignments)
1489.236 Million cell updates/sec

Title: US-10-506-624-2
Perfect score: 3257
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 622

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	3130.5	96.1	603	2 US-09-961-679-2	Sequence 2, Appli
2	1826.5	56.1	353	2 US-09-961-679-6	Sequence 6, Appli
3	1657	50.9	316	2 US-09-961-679-4	Sequence 4, Appli
4	528	16.2	222	2 US-09-270-767-41682	Sequence 41682, A
5	528	16.2	222	2 US-09-270-767-56927	Sequence 56927, A
6	250	7.7	539	2 US-09-701-068-2	Sequence 2, Appli
7	233	7.2	474	2 US-09-701-068-5	Sequence 5, Appli
8	210	6.4	325	2 US-09-489-039A-13618	Sequence 13618, A
9	167.5	5.1	355	2 US-09-543-681A-5929	Sequence 5929, Ap
10	166.5	5.1	357	2 US-09-270-767-32690	Sequence 32690, A

11	166.5	5.1	357	2	US-09-270-767-47907	Sequence 47907, A
12	145	4.5	97	2	US-09-270-767-31865	Sequence 31865, A
13	135	4.1	333	2	US-09-270-767-32349	Sequence 32349, A
14	135	4.1	333	2	US-09-270-767-47566	Sequence 47566, A
15	133.5	4.1	508	2	US-09-248-796A-20809	Sequence 20809, A
16	125	3.8	168	2	US-09-248-796A-20808	Sequence 20808, A
17	116	3.6	634	2	US-09-489-039A-8399	Sequence 8399, Ap
18	116	3.6	634	2	US-09-949-016-7542	Sequence 7542, Ap
19	112.5	3.5	921	1	US-08-568-459A-8	Sequence 8, Appli
20	112.5	3.5	921	1	US-08-487-826B-8	Sequence 8, Appli
21	112.5	3.5	921	2	US-09-210-288-8	Sequence 8, Appli
22	112.5	3.5	921	2	US-10-153-273-8	Sequence 8, Appli
23	110.5	3.4	555	2	US-10-104-047-3369	Sequence 3369, Ap
24	109.5	3.4	324	2	US-09-605-703B-1356	Sequence 1356, Ap
25	109	3.3	1291	2	US-08-704-159-40	Sequence 40, Appl
26	107.5	3.3	872	2	US-09-949-016-8039	Sequence 8039, Ap
27	107.5	3.3	872	2	US-09-949-016-8040	Sequence 8040, Ap
28	107.5	3.3	872	2	US-09-949-016-8041	Sequence 8041, Ap
29	107.5	3.3	872	2	US-09-949-016-8042	Sequence 8042, Ap
30	105.5	3.2	486	2	US-09-328-352-6007	Sequence 6007, Ap
31	105	3.2	292	2	US-09-543-681A-7272	Sequence 7272, Ap
32	104	3.2	318	2	US-09-270-767-44026	Sequence 44026, A
33	103.5	3.2	403	2	US-09-489-039A-9921	Sequence 9921, Ap
34	103	3.2	197	2	US-09-385-219A-32	Sequence 32, Appl
35	103	3.2	723	2	US-09-248-796A-15245	Sequence 15245, A
36	102.5	3.1	1444	2	US-09-949-016-9652	Sequence 9652, Ap
37	102.5	3.1	2004	2	US-09-538-092-1371	Sequence 1371, Ap
38	102.5	3.1	2004	2	US-09-949-016-6756	Sequence 6756, Ap
39	100	3.1	265	2	US-09-154-083-8	Sequence 8, Appli
40	99.5	3.1	344	1	US-08-689-974-1	Sequence 1, Appli
41	99.5	3.1	344	2	US-09-058-376-1	Sequence 1, Appli
42	99.5	3.1	500	2	US-09-489-039A-10995	Sequence 10995, A
43	99	3.0	285	2	US-09-248-796A-18821	Sequence 18821, A
44	98.5	3.0	474	2	US-09-949-016-7983	Sequence 7983, Ap
45	98.5	3.0	474	2	US-09-949-016-7984	Sequence 7984, Ap

Search completed: August 5, 2006, 11:36:36
 Job time : 37.5584 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 5, 2006, 11:36:48 ; Search time 21.3257 Seconds
(without alignments)
1951.660 Million cell updates/sec

Title: US-10-506-624-2
Perfect score: 3257
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 622

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 236815 seqs, 66914042 residues

Total number of hits satisfying chosen parameters: 236815

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
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2	338	10.4	636	6	US-10-953-349-32706	Sequence 32706, A
3	338	10.4	636	7	US-11-056-355B-63281	Sequence 63281, A
4	338	10.4	690	6	US-10-953-349-32705	Sequence 32705, A
5	338	10.4	690	7	US-11-056-355B-63280	Sequence 63280, A
6	319	9.8	494	6	US-10-953-349-32707	Sequence 32707, A
7	319	9.8	494	7	US-11-056-355B-63282	Sequence 63282, A
8	291.5	8.9	559	7	US-11-056-355B-72751	Sequence 72751, A
9	286.5	8.8	570	6	US-10-953-349-6076	Sequence 6076, Ap

10	286.5	8.8	570	7	US-11-056-355B-29539	Sequence 29539, A
11	286.5	8.8	570	7	US-11-056-355B-33129	Sequence 33129, A
12	280	8.6	528	7	US-11-056-355B-87545	Sequence 87545, A
13	279.5	8.6	545	7	US-11-056-355B-81068	Sequence 81068, A
14	279.5	8.6	580	7	US-11-056-355B-81067	Sequence 81067, A
15	279.5	8.6	643	7	US-11-056-355B-81066	Sequence 81066, A
16	278.5	8.6	597	6	US-10-449-902-53836	Sequence 53836, A
17	253.5	7.8	523	6	US-10-449-902-44629	Sequence 44629, A
18	239	7.3	430	6	US-10-953-349-6077	Sequence 6077, Ap
19	239	7.3	430	7	US-11-056-355B-29540	Sequence 29540, A
20	239	7.3	430	7	US-11-056-355B-33130	Sequence 33130, A
21	192.5	5.9	406	7	US-11-056-355B-72752	Sequence 72752, A
22	181	5.6	375	7	US-11-056-355B-87546	Sequence 87546, A
23	180	5.5	1084	6	US-10-449-902-41128	Sequence 41128, A
24	152.5	4.7	265	6	US-10-449-902-39371	Sequence 39371, A
25	152.5	4.7	310	6	US-10-953-349-6078	Sequence 6078, Ap
26	152.5	4.7	310	7	US-11-056-355B-29541	Sequence 29541, A
27	152.5	4.7	310	7	US-11-056-355B-33131	Sequence 33131, A
28	105.5	3.2	364	7	US-11-056-355B-20081	Sequence 20081, A
29	105.5	3.2	382	7	US-11-056-355B-20080	Sequence 20080, A
30	105.5	3.2	405	7	US-11-056-355B-20079	Sequence 20079, A
31	104.5	3.2	694	6	US-10-449-902-44880	Sequence 44880, A
32	103	3.2	197	7	US-11-106-014-32	Sequence 32, Appl
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34	100.5	3.1	881	7	US-11-056-355B-71614	Sequence 71614, A
35	99	3.0	197	7	US-11-056-355B-64591	Sequence 64591, A
36	99	3.0	550	7	US-11-056-355B-105675	Sequence 105675,
37	99	3.0	550	7	US-11-056-355B-116914	Sequence 116914,
38	98	3.0	26	7	US-11-134-871-414	Sequence 414, App
39	98	3.0	810	7	US-11-056-355B-107092	Sequence 107092,
40	98	3.0	810	7	US-11-056-355B-118331	Sequence 118331,
41	98	3.0	821	7	US-11-056-355B-107091	Sequence 107091,
42	98	3.0	821	7	US-11-056-355B-118330	Sequence 118330,
43	98	3.0	945	7	US-11-056-355B-107090	Sequence 107090,
44	98	3.0	945	7	US-11-056-355B-118329	Sequence 118329,
45	95	2.9	612	7	US-11-056-355B-97133	Sequence 97133, A

Search completed: August 5, 2006, 11:41:40
 Job time : 23.3257 secs

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OM protein - protein search, using sw model

Run on: August 5, 2006, 11:28:08 ; Search time 27.4188 Seconds
 (without alignments)
 2182.695 Million cell updates/sec

Title: US-10-506-624-2
 Perfect score: 3257
 Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLMPCREDD 622

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
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2	932.5	28.6	591	2	T19746	hypothetical prote
3	923.5	28.4	1199	2	S20969	Na+/Ca2+, K+-exchan
4	866.5	26.6	611	2	T21747	hypothetical prote
5	388.5	11.9	590	2	S40707	hypothetical prote
6	376	11.5	743	2	T38674	probable membrane
7	331.5	10.2	651	2	T03889	Na+/Ca2+, K+-exchan
8	294	9.0	546	2	D86221	hypothetical prote
9	294	9.0	703	2	T03888	Na+/Ca2+, K+-exchan
10	291	8.9	644	2	B96582	hypothetical prote
11	280	8.6	807	2	T24110	hypothetical prote
12	264	8.1	591	2	S40705	Na+/Ca2+, K+-exchan
13	255	7.8	433	2	S74922	hypothetical prote

14	253.5	7.8	538	2	T00424	probable Na ⁺ /Ca ²⁺
15	248.5	7.6	332	2	H82064	conserved hypothet
16	247.5	7.6	330	2	H69020	probable Na ⁺ /Ca ²⁺ ,
17	243	7.5	762	2	S67765	probable membrane
18	234	7.2	890	2	B89047	protein C10G8.5 [i
19	232.5	7.1	302	2	C64311	Na ⁺ /Ca ²⁺ -exchangin
20	227.5	7.0	941	2	B53335	Na ⁺ /Ca ²⁺ -exchangin
21	224	6.9	318	2	A83708	hypothetical prote
22	222.5	6.8	935	2	S43730	Na ⁺ /Ca ²⁺ -exchangin
23	218	6.7	921	2	A54139	Na ⁺ /Ca ²⁺ -exchangin
24	217.5	6.7	344	2	E84376	Na ⁺ /Ca ²⁺ -exchangin
25	217.5	6.7	957	2	A53789	Na ⁺ /Ca ²⁺ -exchangin
26	216.5	6.6	322	2	E69009	cation antiporter
27	216	6.6	958	2	S32435	Na ⁺ /Ca ²⁺ -exchangin
28	214	6.6	324	2	AI0434	probable sodium/ca
29	212	6.5	970	2	I48097	Na ⁺ /Ca ²⁺ -exchangin
30	209	6.4	325	2	AI0904	probable membrane
31	209	6.4	970	2	A36417	Na ⁺ /Ca ²⁺ -exchangin
32	209	6.4	973	2	S32815	Na ⁺ /Ca ²⁺ -exchangin
33	207	6.4	325	2	C91138	hypothetical prote
34	207	6.4	325	2	F85983	hypothetical prote
35	206	6.3	325	2	F65110	hypothetical 34.7
36	206	6.3	400	2	T49810	hypothetical prote
37	204.5	6.3	971	2	S28833	Na ⁺ /Ca ²⁺ -exchangin
38	202	6.2	309	2	B72342	conserved hypothet
39	192	5.9	314	2	C75003	na ⁺ /ca ⁺ exchanging
40	188	5.8	970	2	S27114	Na ⁺ /Ca ²⁺ -exchangin
41	184	5.6	322	2	E70306	conserved hypothet
42	182	5.6	325	2	D71159	probable Na ⁺ /Ca ²⁺ -
43	172.5	5.3	160	2	T45258	hypothetical prote
44	167	5.1	158	2	S68978	Na ⁺ /Ca ²⁺ ,K ⁺ -exchan
45	160	4.9	341	2	A71250	conserved hypothet

Search completed: August 5, 2006, 11:35:22
Job time : 30.4188 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 5, 2006, 11:35:38 ; Search time 126.939 Seconds
(without alignments)
2269.753 Million cell updates/sec

Title: US-10-506-624-2
Perfect score: 3257
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 622

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3257	100.0	622	5	US-10-506-624-2
2	3130.5	96.1	603	3	US-09-961-679-2
3	3130.5	96.1	603	5	US-10-886-518-2
4	3130.5	96.1	603	5	US-10-506-624-4
5	1867.5	57.3	644	4	US-10-353-690-18
6	1852	56.9	480	5	US-10-450-763-42982
7	1826.5	56.1	353	3	US-09-961-679-6
8	1826.5	56.1	353	5	US-10-886-518-6
9	1683.5	51.7	352	4	US-10-108-260A-3558
10	1657	50.9	316	3	US-09-961-679-4
11	1657	50.9	316	5	US-10-886-518-4

12	1051.5	32.3	661	4	US-10-094-214-5	Sequence 5, Appli
13	1051.5	32.3	661	4	US-10-281-868-2	Sequence 2, Appli
14	1051.5	32.3	661	4	US-10-391-399-17	Sequence 17, Appl
15	998	30.6	856	6	US-11-097-143-8067	Sequence 8067, Ap
16	986	30.3	658	6	US-11-097-143-252	Sequence 252, App
17	954	29.3	500	4	US-10-264-104-2	Sequence 2, Appli
18	944.5	29.0	1081	4	US-10-408-765A-298	Sequence 298, App
19	932.5	28.6	591	4	US-10-369-493-6463	Sequence 6463, Ap
20	932.5	28.6	591	4	US-10-369-493-6464	Sequence 6464, Ap
21	907.5	27.9	235	3	US-09-985-153-133	Sequence 133, App
22	866.5	26.6	611	4	US-10-369-493-5204	Sequence 5204, Ap
23	837	25.7	169	3	US-09-985-153-90	Sequence 90, Appl
24	837	25.7	169	5	US-10-472-533-588	Sequence 588, App
25	773	23.7	481	6	US-11-097-143-3162	Sequence 3162, Ap
26	723	22.2	137	5	US-10-450-763-42981	Sequence 42981, A
27	703.5	21.6	168	3	US-09-985-153-69	Sequence 69, Appl
28	703.5	21.6	168	5	US-10-472-533-475	Sequence 475, App
29	693	21.3	168	3	US-09-798-889-51	Sequence 51, Appl
30	693	21.3	168	4	US-10-633-680-51	Sequence 51, Appl
31	635	19.5	353	6	US-11-097-143-1746	Sequence 1746, Ap
32	387.5	11.9	227	4	US-10-264-104-5	Sequence 5, Appli
33	372.5	11.4	362	6	US-11-097-143-38151	Sequence 38151, A
34	355	10.9	584	4	US-10-168-651-5	Sequence 5, Appli
35	350	10.7	584	4	US-10-094-214-2	Sequence 2, Appli
36	350	10.7	584	4	US-10-391-399-14	Sequence 14, Appl
37	338	10.4	636	6	US-11-096-568A-12978	Sequence 12978, A
38	338	10.4	690	6	US-11-096-568A-12977	Sequence 12977, A
39	334.5	10.3	585	6	US-11-012-762-6	Sequence 6, Appli
40	319	9.8	494	6	US-11-096-568A-12979	Sequence 12979, A
41	310.5	9.5	489	4	US-10-437-963-190947	Sequence 190947,
42	305	9.4	329	5	US-10-506-454-951	Sequence 951, App
43	300.5	9.2	634	4	US-10-425-115-317894	Sequence 317894,
44	296.5	9.1	575	4	US-10-437-963-201523	Sequence 201523,
45	293	9.0	560	6	US-11-097-143-36060	Sequence 36060, A

ALIGNMENTS

RESULT 1

US-10-506-624-2

; Sequence 2, Application US/10506624

; Publication No. US20050119173A1

; GENERAL INFORMATION:

; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.

; TITLE OF INVENTION: Novel potassium-dependent sodium/calcium exchanger

; FILE REFERENCE: Y0335PCT-693

; CURRENT APPLICATION NUMBER: US/10/506,624

; CURRENT FILING DATE: 2004-09-03

; PRIOR APPLICATION NUMBER: JP 2002-225114

; PRIOR FILING DATE: 2002-08-01

; PRIOR APPLICATION NUMBER: JP 2003-182989

; PRIOR FILING DATE: 2003-06-26

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 622

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-506-624-2

Query Match 100.0%; Score 3257; DB 5; Length 622;
Best Local Similarity 100.0%; Pred. No. 5.4e-275;
Matches 622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MALRGTLRPLKVRRRREMLPQQVGFCVAVLALVCCASGLFGSLGHKTASASKRVLPDTWR 60

Qy     61 NRKLMAVPNGTQTAKNCTDPAIHEFPTDLFSNKERQHGA VLLHILGALYMFYALAIVCDD 120
Db     61 NRKLMAVPNGTQTAKNCTDPAIHEFPTDLFSNKERQHGA VLLHILGALYMFYALAIVCDD 120

Qy    121 FFVPSLEKICERLHLS EDVAGATFMAAGSSTPELFASVIGVFITHGDVGVGTIVGSAVFN 180
Db    121 FFVPSLEKICERLHLS EDVAGATFMAAGSSTPELFASVIGVFITHGDVGVGTIVGSAVFN 180

Qy    181 ILCIIGVCGLFAGQVVRLTWWAVCRDSVYYTISVIVLIVFIYDEQIVWWEGVLIIILYVF 240
Db    181 ILCIIGVCGLFAGQVVRLTWWAVCRDSVYYTISVIVLIVFIYDEQIVWWEGVLIIILYVF 240

Qy    241 YILIMKYNVKMQAFFTVKQKSIANGNPVNSELEAGNDFYDGSYDDPSVPLLGQVKEKPQY 300
Db    241 YILIMKYNVKMQAFFTVKQKSIANGNPVNSELEAGNDFYDGSYDDPSVPLLGQVKEKPQY 300

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Db    301 GKNPVVMVDEIMSSSPPKFTFPEAGLRIMITNKFGRPRTRLRMASRIIINERQRLINSANG 360

Qy    361 VSSKPLQNGRHENIENG NVPVENPEDPQQNQEQQPPPPQPPPEPEPEVEADFLSPFSVPEA 420
Db    361 VSSKPLQNGRHENIENG NVPVENPEDPQQNQEQQPPPPQPPPEPEPEVEADFLSPFSVPEA 420

Qy    421 RGDVKVWVFTWPLIFLLCVTIPNCSKPRWEKFFMVTFITATLWIAVFSYIMVWLVTIIGY 480
Db    421 RGDVKVWVFTWPLIFLLCVTIPNCSKPRWEKFFMVTFITATLWIAVFSYIMVWLVTIIGY 480

Qy    481 TLGIPDVIMGITFLAAGTSVPDCMASLIVARQGLGDMAVSNTIGSNVFDILVGLGVPWGL 540
Db    481 TLGIPDVIMGITFLAAGTSVPDCMASLIVARQGLGDMAVSNTIGSNVFDILVGLGVPWGL 540

Qy    541 QTMVVNYGSTVKINSRGLVYSVLLLLGSVALTVLGIHLNWKRLDRKLG VYVLVLYAIFLC 600
Db    541 QTMVVNYGSTVKINSRGLVYSVLLLLGSVALTVLGIHLNWKRLDRKLG VYVLVLYAIFLC 600

Qy    601 FSIMIEFNVFTFVNLP MCREDD 622
Db    601 FSIMIEFNVFTFVNLP MCREDD 622
```

RESULT 2

US-09-961-679-2

; Sequence 2, Application US/09961679

; Patent No. US20020107380A1

```
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Gerhardt, Brenda
; TITLE OF INVENTION: No. US20020107380A1e1 Human Ion-Exchanger Proteins and
Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0239-USA
; CURRENT APPLICATION NUMBER: US/09/961,679
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/235,745
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 603
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-961-679-2
```

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Query Match          96.1%; Score 3130.5; DB 3; Length 603;
Best Local Similarity 96.9%; Pred. No. 5.6e-264;
Matches 603; Conservative 0; Mismatches 0; Indels 19; Gaps 1;
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Qy      1 MALRGTLRPLKVRRRREMLPQQVGFVCAVLALVCCASGLFGSLGHKTASASKRVLPDTPWR 60
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Db      1 MALRGTLRPLKVRRRREMLPQQVGFVCAVLALVCCASGLFGSLGHKTASASKRVLPDTPWR 60

Qy     61 NRKLMAPVNGTQTAKNCTDPAIHEFPTDLFSNKERQHGAVLLHILGALYMFYALAIVCDD 120
      |||
Db     61 NRKLMAPVNGTQTAKNCTDPAIHEFPTDLFSNKERQHGAVLLHILGALYMFYALAIVCDD 120

Qy    121 FFVPSLEKICERLHLSEDVAGATFMAAGSSSTPELFASVIGVFITHGDVGVTIVGSAVFN 180
      |||
Db    121 FFVPSLEKICERLHLSEDVAGATFMAAGSSSTPELFASVIGVFITHGDVGVTIVGSAVFN 180

Qy    181 ILCIIGVCGLFAGQVVRLTWWAVCRDSVYYTISVIVLIVFIYDEQIVWWEGLVLIILYVF 240
      |||
Db    181 ILCIIGVCGLFAGQVVRLTWWAVCRDSVYYTISVIVLIVFIYDEQIVWWEGLVLIILYVF 240

Qy    241 YILIMKYNVKMQAFFTVKQKSIANGNPVNSELEAGNDFYDGSYDDPSVPLLQVKEKPQY 300
      |||
Db    241 YILIMKYNVKMQAFFTVKQKSIANGNPVNSELEA-----VKEKPQY 281

Qy    301 GKNPVVMVDEIMSSSPPKFTFPEAGLRIMITNKFGPRTLRLMASRIIINERQRLINSANG 360
      |||
Db    282 GKNPVVMVDEIMSSSPPKFTFPEAGLRIMITNKFGPRTLRLMASRIIINERQRLINSANG 341

Qy    361 VSSKPLQNGRHENIENGVPVENPEDPQQNQEQQPPPPQPPPEPEPVEADFLSPFSVPEA 420
      |||
Db    342 VSSKPLQNGRHENIENGVPVENPEDPQQNQEQQPPPPQPPPEPEPVEADFLSPFSVPEA 401

Qy    421 RGDVKVWVFTWPLIFLLCVTIPNCSKPRWEKFFMVTFITATLWIAVFSYIMVWLVTIIGY 480
      |||
Db    402 RGDVKVWVFTWPLIFLLCVTIPNCSKPRWEKFFMVTFITATLWIAVFSYIMVWLVTIIGY 461

Qy    481 TLGIPDVIMGITFLAAGTSVPDCMASLIVARQGLGDMAVSNTIGSNVFDILVGLGVPWGL 540
      |||
```



```

      |||
Db      241 YILIMKYNVKMQAFFTVKQKSIANGNPVNSELEA-----VKEKPQY 281
      |||
Qy      301 GKNPVVMVDEIMSSSPPKFTFPEAGLRIMITNKFGPRTRLRMASRIIINERQRLINSANG 360
      |||
Db      282 GKNPVVMVDEIMSSSPPKFTFPEAGLRIMITNKFGPRTRLRMASRIIINERQRLINSANG 341
      |||
Qy      361 VSSKPLQNGRHENIENGNNVPVENPEDPQQNQEQQPPPPQPPPEPEPVEADFLSPFSVPEA 420
      |||
Db      342 VSSKPLQNGRHENIENGNNVPVENPEDPQQNQEQQPPPPQPPPEPEPVEADFLSPFSVPEA 401
      |||
Qy      421 RGDVKVWVFTWPLIFLLCVTIPNCSKPRWEKFFMVTFITATLWIAVFSYIMVWLVTIIGY 480
      |||
Db      402 RGDVKVWVFTWPLIFLLCVTIPNCSKPRWEKFFMVTFITATLWIAVFSYIMVWLVTIIGY 461
      |||
Qy      481 TLGIPDVIMGITFLAAGTSVPDCMASLIVARQGLGDMASNTIGSNVFDILVGLGVPWGL 540
      |||
Db      462 TLGIPDVIMGITFLAAGTSVPDCMASLIVARQGLGDMASNTIGSNVFDILVGLGVPWGL 521
      |||
Qy      541 QTMVVNYGSTVKINSRGLVYSVLLLGSAVLTVLGIHLNWKWRLDRKLG VYVLVLYAIFLC 600
      |||
Db      522 QTMVVNYGSTVKINSRGLVYSVLLLGSAVLTVLGIHLNWKWRLDRKLG VYVLVLYAIFLC 581
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Qy      601 FSIMIEFNVTFTVNLPMCREDD 622
      |||
Db      582 FSIMIEFNVTFTVNLPMCREDD 603

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RESULT 4

US-10-506-624-4

; Sequence 4, Application US/10506624

; Publication No. US20050119173A1

; GENERAL INFORMATION:

; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.

; TITLE OF INVENTION: Novel potassium-dependent sodium/calcium exchanger

; FILE REFERENCE: Y0335PCT-693

; CURRENT APPLICATION NUMBER: US/10/506,624

; CURRENT FILING DATE: 2004-09-03

; PRIOR APPLICATION NUMBER: JP 2002-225114

; PRIOR FILING DATE: 2002-08-01

; PRIOR APPLICATION NUMBER: JP 2003-182989

; PRIOR FILING DATE: 2003-06-26

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 603

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-506-624-4

Query Match 96.1%; Score 3130.5; DB 5; Length 603;

Best Local Similarity 96.9%; Pred. No. 5.6e-264;

Matches 603; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

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Qy      1 MALRGTLRPLKVRRRREMLPQQVG FVCAVLALVCCASGLFGSLGHKTASASKRVLPD TWR 60
      |||
Db      1 MALRGTLRPLKVRRRREMLPQQVG FVCAVLALVCCASGLFGSLGHKTASASKRVLPD TWR 60

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```
Qy      61 NRKLMA PVNGTQTAKNCTDPAIHEFPTDLFSN KERQHGAVLLHILGALYMFYALAIVCDD 120
      |||
Db      61 NRKLMA PVNGTQTAKNCTDPAIHEFPTDLFSN KERQHGAVLLHILGALYMFYALAIVCDD 120

Qy     121 FFVPSLEKICERLHLS EDVAGATFMAAGSSTPELFASVIGVFITHGDVGVGTIVGSAVFN 180
      |||
Db     121 FFVPSLEKICERLHLS EDVAGATFMAAGSSTPELFASVIGVFITHGDVGVGTIVGSAVFN 180

Qy     181 ILCIIGVCGLFAGQVVR LTTWAVCRDSVYYTISVIVLIVFIYDEQIVWWEGLVLIILYVF 240
      |||
Db     181 ILCIIGVCGLFAGQVVR LTTWAVCRDSVYYTISVIVLIVFIYDEQIVWWEGLVLIILYVF 240

Qy     241 YILIMKYNVKMQAFFTVKQKSIANGNPVNSELEAGNDFYDGSYDDPSVPLLQGVKEKPQY 300
      |||
Db     241 YILIMKYNVKMQAFFTVKQKSIANGNPVNSELEA-----VKEKPQY 281

Qy     301 GKNPVVMVDEIMSSSPKFTFPEAGLRIMITNKFGPRTRLRMASRIIINERQRLINSANG 360
      |||
Db     282 GKNPVVMVDEIMSSSPKFTFPEAGLRIMITNKFGPRTRLRMASRIIINERQRLINSANG 341

Qy     361 VSSKPLQNGRHENIENG NVPVENPEDPQQNQEQPPPPQPPPEPEPEVEADFLSPFSVPEA 420
      |||
Db     342 VSSKPLQNGRHENIENG NVPVENPEDPQQNQEQPPPPQPPPEPEPEVEADFLSPFSVPEA 401

Qy     421 RGDVKVWVFTWPLIFLLCVTIPNCSKPRWEKFFMVTFITATLWIAVFSYIMVWLVTIIGY 480
      |||
Db     402 RGDVKVWVFTWPLIFLLCVTIPNCSKPRWEKFFMVTFITATLWIAVFSYIMVWLVTIIGY 461

Qy     481 TLGIPDVIMGITFLAAGTSVPDCMASLIVARQGLGDMAVSNTIGSNVFDILVGLGVPWGL 540
      |||
Db     462 TLGIPDVIMGITFLAAGTSVPDCMASLIVARQGLGDMAVSNTIGSNVFDILVGLGVPWGL 521

Qy     541 QTMVVNYGSTVKINSRGLVYSV VLLLSGVALTVLGIHLNKNWRLDRKLG VYVLVLYAIFLC 600
      |||
Db     522 QTMVVNYGSTVKINSRGLVYSV VLLLSGVALTVLGIHLNKNWRLDRKLG VYVLVLYAIFLC 581

Qy     601 FSIMIEFN VFTFVNLP MCREDD 622
      |||
Db     582 FSIMIEFN VFTFVNLP MCREDD 603
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Search completed: August 5, 2006, 11:40:52
Job time : 127.939 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 5, 2006, 15:40:21 ; Search time 8199.74 Seconds
(without alignments)
7276.202 Million cell updates/sec

Title: US-10-506-624-2
Perfect score: 3257
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMCREDD 622

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10506624/runat_04082006_171933_9039/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10506624_@CGN_1_1_12389_@runat_04082006_171933_9039 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*

13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3212	98.6	1892	5	BC069653	BC069653 Homo sapi
2	3212	98.6	4467	5	AF520704	AF520704 Homo sapi
3	3130.5	96.1	1812	2	AR580276	AR580276 Sequence
4	3130.5	96.1	1812	2	AX406625	AX406625 Sequence
5	3130.5	96.1	2366	2	AR580279	AR580279 Sequence
6	3130.5	96.1	2366	2	AX406631	AX406631 Sequence
7	3085.5	94.7	4410	5	AF520705	AF520705 Homo sapi
8	3069	94.2	2094	6	AY156046	AY156046 Mus muscu
9	3045	93.5	4419	5	AF520706	AF520706 Homo sapi
10	2476.5	76.0	4206	5	HSM809146	BX648995 Homo sapi
11	2010.5	61.7	2178	11	BC093185	BC093185 Danio rer
12	1867.5	57.3	3763	2	DD200094	DD200094 Methods a
13	1866.5	57.3	3905	5	AF288087	AF288087 Homo sapi
14	1852.5	56.9	3637	5	AF169257	AF169257 Homo sapi
15	1845	56.6	2392	6	AF314821	AF314821 Mus muscu
16	1842.5	56.6	1937	6	AY009158	AY009158 Rattus no
17	1838.5	56.4	3436	6	BC017615	BC017615 Mus muscu
18	1832.5	56.3	2296	2	CS167870	CS167870 Sequence
19	1832.5	56.3	2296	2	AX833991	AX833991 Sequence
20	1832.5	56.3	2296	5	AK096171	AK096171 Homo sapi
21	1826.5	56.1	1062	2	AR580278	AR580278 Sequence
22	1826.5	56.1	1062	2	AX406629	AX406629 Sequence
23	1823	56.0	2036	2	AR578596	AR578596 Sequence
24	1728	53.1	4766	5	HSM805663	AL834225 Homo sapi
25	1657	50.9	951	2	AR580277	AR580277 Sequence
26	1657	50.9	951	2	AX406627	AX406627 Sequence
27	1544	47.4	1041	2	CQ719073	CQ719073 Sequence
28	1267	38.9	955	11	CR386930	CR386930 Gallus ga
29	1056	32.4	2170	5	AF177987	AF177987 Homo sapi
30	1051.5	32.3	2086	5	BC069622	BC069622 Homo sapi
31	1051.5	32.3	2221	5	AF097366	AF097366 Homo sapi
32	1046.5	32.1	2194	2	BD269311	BD269311 33 human
33	1037	31.8	2182	11	AF177986	AF177986 Gallus ga
34	1033	31.7	8942	6	AF021923	AF021923 Rattus no
35	1032.5	31.7	2016	13	AY084156	AY084156 Drosophil
36	1030.5	31.6	2120	11	AF177985	AF177985 Gallus ga
37	1026.5	31.5	2259	11	AF177984	AF177984 Gallus ga
38	1009.5	31.0	3308	2	BD269290	BD269290 33 human
39	1009	31.0	3306	2	BD269310	BD269310 33 human
40	1005	30.9	2565	6	BC005742	BC005742 Mus muscu

Search completed: August 5, 2006, 20:14:57
 Job time : 8258.74 secs

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 5, 2006, 15:09:07 ; Search time 1022.62 Seconds
(without alignments)
6361.225 Million cell updates/sec

Title: US-10-506-624-2
Perfect score: 3257
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 622

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10506624/runat_04082006_171931_9028/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
-USER=US10506624 @CGN_1_1_1350 @runat_04082006_171931_9028 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*

13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3257	100.0	1902	12	ADJ65160	Adj65160 Potassium
2	3130.5	96.1	1812	6	AAD35144	Aad35144 Human nov
3	3130.5	96.1	1845	12	ADJ65162	Adj65162 Potassium
4	3130.5	96.1	2366	6	AAD35147	Aad35147 Human nov
5	1867.5	57.3	3763	10	ADE31660	Ade31660 Human 692
6	1867.5	57.3	3874	14	ADX38783	Adx38783 Human can
7	1867.5	57.3	3889	14	ADX38781	Adx38781 Human can
8	1867.5	57.3	3919	14	ADX38784	Adx38784 Human can
9	1866.5	57.3	3828	14	ADX38670	Adx38670 Human can
10	1852	56.9	1443	5	AAS76810	Aas76810 DNA encod
11	1845	56.6	3577	14	ADX38588	Adx38588 Human can
12	1845	56.6	3577	14	ADX38675	Adx38675 Human can
13	1832.5	56.3	2296	11	ADM02430	Adm02430 Human cDN
14	1832.5	56.3	2296	14	AEC85360	Aec85360 Human cDN
15	1826.5	56.1	1062	6	AAD35146	Aad35146 Human nov
16	1823	56.0	2036	6	ABZ11890	Abz11890 Human pol
17	1823	56.0	2036	12	ADM44408	Adm44408 Novel hum
18	1657	50.9	951	6	AAD35145	Aad35145 Human nov
19	1051.5	32.3	2221	8	AAL60325	Aal60325 Human 577
20	1051.5	32.3	2221	14	ADZ49507	Adz49507 Insulin s
21	1051.5	32.3	2513	4	AAK51845	Aak51845 Human pol
22	1046.5	32.1	2194	3	AAA87702	Aaa87702 Human sec
23	1046.5	32.1	2194	8	ADA40550	Ada40550 Human sec
24	1046.5	32.1	2194	8	ACC50853	Acc50853 Human sec
25	1046.5	32.1	2194	8	ABZ71478	Abz71478 Secreted
26	1046.5	32.1	2194	9	ADB91445	Adb91445 Human sec
27	1046.5	32.1	2194	10	ADC73985	Adc73985 Human sec
28	1046.5	32.1	2194	10	ADA56696	Ada56696 Gene enco
29	1009.5	31.0	3308	3	AAA87681	Aaa87681 Human sec
30	1009.5	31.0	3308	8	ADA40228	Ada40228 Human sec
31	1009.5	31.0	3308	8	ACC50671	Acc50671 Human sec
32	1009.5	31.0	3308	8	ABZ71365	Abz71365 Secreted
33	1009.5	31.0	3308	9	ADB91306	Adb91306 Human sec
34	1009.5	31.0	3308	10	ADC73754	Adc73754 Human sec
35	1009.5	31.0	3308	10	ADA56388	Ada56388 Gene enco
36	1009	31.0	3306	3	AAA87701	Aaa87701 Human sec
37	1009	31.0	3306	8	ADA40549	Ada40549 Human sec
38	1009	31.0	3306	8	ACC50852	Acc50852 Human sec
39	1009	31.0	3306	8	ABZ71477	Abz71477 Secreted
40	1009	31.0	3306	9	ADB91444	Adb91444 Human sec

Search completed: August 5, 2006, 16:15:55
 Job time : 1038.62 secs

GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 5, 2006, 15:45:16 ; Search time 283.327 Seconds
 (without alignments)
 6161.581 Million cell updates/sec

Title: US-10-506-624-2
 Perfect score: 3257
 Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 622

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
 -Q=/abss/ABSSWEB_spool/US10506624/runat_04082006_171937_9122/app_query.fasta_1
 -DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
 -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -HOST=abss03p -USER=US10506624 @CGN_1_1_381 @runat_04082006_171937_9122
 -NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					Description
	No.	Score	Match Length	DB	ID	
	1	3130.5	96.1	1812	3	US-09-961-679-1
	2	3130.5	96.1	2366	3	US-09-961-679-7
	3	1826.5	56.1	1062	3	US-09-961-679-5
	4	1823	56.0	2036	3	US-09-799-451-772
	5	1657	50.9	951	3	US-09-961-679-3
	6	528	16.2	1174	3	US-09-270-767-25428
	7	528	16.2	1612	3	US-09-270-767-10086
	8	493	15.1	744	3	US-09-976-594-1120
	9	322.5	9.9	2412	3	US-09-799-451-229
c	10	259.5	8.0	1684	3	US-10-104-047-1419
	11	258.5	7.9	1935	3	US-09-701-068-3
	12	258.5	7.9	1950	3	US-09-701-068-1
c	13	232.5	7.1	1664976	3	US-08-916-421B-1
c	14	232.5	7.1	1664976	3	US-09-692-570-1
	15	222	6.8	3431	3	US-09-221-017B-993
	16	221.5	6.8	546	3	US-09-702-705-129
	17	221.5	6.8	546	3	US-09-736-457-129
	18	221.5	6.8	546	3	US-09-614-124B-129
	19	221.5	6.8	546	3	US-09-671-325-129
	20	221.5	6.8	546	3	US-09-589-184-129
	21	221.5	6.8	546	3	US-09-658-824-129
	22	221.5	6.8	546	3	US-10-017-754-129
	23	221.5	6.8	546	3	US-09-651-563-129
	24	221.5	6.8	546	3	US-09-519-642-129
	25	210	6.4	978	3	US-09-489-039A-6447
	26	179	5.5	1071	3	US-09-270-767-1061
	27	179	5.5	1071	3	US-09-270-767-16343
	28	167.5	5.1	1068	3	US-09-543-681A-1757
	29	163	5.0	999	3	US-09-270-767-720
	30	163	5.0	999	3	US-09-270-767-16002
c	31	145	4.5	964	3	US-09-270-767-236
c	32	145	4.5	964	3	US-09-270-767-15518
	33	140.5	4.3	2803	3	US-09-701-068-4
	34	137	4.2	1527	3	US-09-248-796A-6706
c	35	126	3.9	592	3	US-09-669-751-77
	36	125	3.8	507	3	US-09-248-796A-6705
	37	122.5	3.8	52655	3	US-09-949-016-13495
	38	116	3.6	1905	3	US-09-489-039A-1228
	39	116	3.6	4371	3	US-09-949-016-1671
c	40	114	3.5	1987	3	US-09-949-016-1536
	41	111	3.4	1299	3	US-09-603-208A-133
	42	110.5	3.4	2062	3	US-10-104-047-1399
	43	110.5	3.4	3213	3	US-09-949-016-2951
	44	109.5	3.4	1095	4	US-09-605-703B-1355
	45	109.5	3.4	85122	3	US-09-949-016-14693

Search completed: August 5, 2006, 21:02:27
Job time : 1492.33 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 5, 2006, 15:51:16 ; Search time 1937.09 Seconds
(without alignments)
5918.356 Million cell updates/sec

Title: US-10-506-624-2
Perfect score: 3257
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 622

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10506624/runat_04082006_171939_9185/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss07
-USER=US10506624 @CGN_1_1_2380 @runat_04082006_171939_9185 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	3257	100.0	1902	10	US-10-506-624-1	Sequence 1, Appli	
2	3130.5	96.1	1812	3	US-09-961-679-1	Sequence 1, Appli	
3	3130.5	96.1	1812	10	US-10-886-518-1	Sequence 1, Appli	
4	3130.5	96.1	1845	10	US-10-506-624-3	Sequence 3, Appli	
5	3130.5	96.1	2366	3	US-09-961-679-7	Sequence 7, Appli	
6	3130.5	96.1	2366	10	US-10-886-518-7	Sequence 7, Appli	
7	1867.5	57.3	3763	7	US-10-353-690-17	Sequence 17, Appl	
8	1852	56.9	1443	10	US-10-450-763-12614	Sequence 12614, A	
9	1832.5	56.3	2296	7	US-10-108-260A-1115	Sequence 1115, Ap	
10	1826.5	56.1	1062	3	US-09-961-679-5	Sequence 5, Appli	
11	1826.5	56.1	1062	10	US-10-886-518-5	Sequence 5, Appli	
12	1823	56.0	2036	8	US-10-302-172-772	Sequence 772, App	
13	1657	50.9	951	3	US-09-961-679-3	Sequence 3, Appli	
14	1657	50.9	951	10	US-10-886-518-3	Sequence 3, Appli	
15	1051.5	32.3	2221	7	US-10-281-868-1	Sequence 1, Appli	
16	1051.5	32.3	2221	7	US-10-281-868-3	Sequence 3, Appli	
17	1051.5	32.3	2221	10	US-10-887-553A-836	Sequence 836, App	
18	1046.5	32.1	2194	3	US-09-985-153-47	Sequence 47, Appl	
19	1046.5	32.1	2194	10	US-10-472-533-299	Sequence 299, App	
20	1039	31.9	600	13	US-11-060-756-4124	Sequence 4124, Ap	
21	1039	31.9	600	13	US-11-060-756-8396	Sequence 8396, Ap	
22	1009.5	31.0	3308	3	US-09-985-153-26	Sequence 26, Appl	
23	1009.5	31.0	3308	10	US-10-472-533-186	Sequence 186, App	
24	1009	31.0	3306	3	US-09-985-153-46	Sequence 46, Appl	
25	1009	31.0	3306	10	US-10-472-533-298	Sequence 298, App	
26	998	30.6	3575	13	US-11-097-143-8066	Sequence 8066, Ap	
27	995.5	30.6	1683	13	US-11-097-143-3161	Sequence 3161, Ap	
28	991.5	30.4	2359	13	US-11-097-143-251	Sequence 251, App	
29	954	29.3	1503	6	US-10-264-104-3	Sequence 3, Appli	
30	954	29.3	1596	6	US-10-264-104-1	Sequence 1, Appli	
31	893	27.4	3897	16	US-11-136-527-2555	Sequence 2555, Ap	
32	851	26.1	2492	3	US-09-798-889-43	Sequence 43, Appl	
33	851	26.1	2492	8	US-10-633-680-43	Sequence 43, Appl	
c 34	849.5	26.1	7993	13	US-11-097-143-250	Sequence 250, App	
35	848	26.0	1489	3	US-09-798-889-17	Sequence 17, Appl	
36	848	26.0	1489	8	US-10-633-680-17	Sequence 17, Appl	
37	723	22.2	415	10	US-10-450-763-12613	Sequence 12613, A	
38	691	21.2	12663	13	US-11-097-143-3160	Sequence 3160, Ap	
39	639	19.6	1094	13	US-11-097-143-1745	Sequence 1745, Ap	
c 40	582.5	17.9	1359	4	US-09-925-065A-35884	Sequence 35884, A	

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 5, 2006, 16:10:57 ; Search time 270.633 Seconds
(without alignments)
5460.220 Million cell updates/sec

Title: US-10-506-624-2
Perfect score: 3257
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 622

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2193277 seqs, 791917567 residues

Total number of hits satisfying chosen parameters: 4386554

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10506624/runat_04082006_171941_9232/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss04
-USER=US10506624 @CGN_1_1_306 @runat_04082006_171941_9232 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	1832.5	56.3	2296	8	US-11-293-697-1115	Sequence 1115, Ap
	2	954	29.3	1617	8	US-11-266-748A-23635	Sequence 23635, A
	3	954	29.3	1617	8	US-11-266-748A-31757	Sequence 31757, A
c	4	551	16.9	554	8	US-11-266-748A-354597	Sequence 354597,
	5	551	16.9	554	8	US-11-266-748A-437976	Sequence 437976,
	6	484.5	14.9	1000	8	US-11-266-748A-401181	Sequence 401181,
c	7	484.5	14.9	1000	8	US-11-266-748A-472227	Sequence 472227,
	8	364	11.2	2993	8	US-11-266-748A-30769	Sequence 30769, A
	9	338	10.4	2140	6	US-10-953-349-32704	Sequence 32704, A
	10	338	10.4	2140	7	US-11-056-355B-63279	Sequence 63279, A
	11	308.5	9.5	3033	7	US-11-218-305-12786	Sequence 12786, A
c	12	308	9.5	1670	8	US-11-266-748A-188993	Sequence 188993,
	13	308	9.5	1670	8	US-11-266-748A-242690	Sequence 242690,
	14	306	9.4	1896	6	US-10-449-902-25496	Sequence 25496, A
	15	291.5	8.9	1680	7	US-11-056-355B-72750	Sequence 72750, A
	16	286.5	8.8	1871	6	US-10-953-349-6075	Sequence 6075, Ap
	17	286.5	8.8	1871	7	US-11-056-355B-29538	Sequence 29538, A
	18	286.5	8.8	1871	7	US-11-056-355B-33128	Sequence 33128, A
	19	280	8.6	1587	7	US-11-056-355B-87544	Sequence 87544, A
	20	279.5	8.6	1932	7	US-11-056-355B-81065	Sequence 81065, A
	21	265	8.1	1969	6	US-10-449-902-16206	Sequence 16206, A
	22	257.5	7.9	2295	8	US-11-217-529-2812	Sequence 2812, Ap
	23	221.5	6.8	546	8	US-11-301-554-129	Sequence 129, App
	24	221.5	6.8	680	8	US-11-266-748A-212830	Sequence 212830,
c	25	221.5	6.8	680	8	US-11-266-748A-236131	Sequence 236131,
	26	217.5	6.7	735	8	US-11-266-748A-255563	Sequence 255563,
c	27	217.5	6.7	735	8	US-11-266-748A-316080	Sequence 316080,
	28	217.5	6.7	1507	8	US-11-266-748A-81568	Sequence 81568, A
c	29	217.5	6.7	1507	8	US-11-266-748A-134379	Sequence 134379,
c	30	207	6.4	3632	7	US-11-218-305-21414	Sequence 21414, A
	31	207	6.4	4282	8	US-11-266-748A-56894	Sequence 56894, A
	32	180.5	5.5	3646	6	US-10-449-902-12682	Sequence 12682, A
	33	175.5	5.4	2172	8	US-11-217-529-3060	Sequence 3060, Ap
c	34	171	5.3	1109	8	US-11-266-748A-355575	Sequence 355575,
	35	171	5.3	1109	8	US-11-266-748A-438954	Sequence 438954,
	36	171	5.3	1436	8	US-11-266-748A-76380	Sequence 76380, A
c	37	171	5.3	1436	8	US-11-266-748A-129191	Sequence 129191,
	38	164.5	5.1	1000	8	US-11-266-748A-223147	Sequence 223147,
	39	164.5	5.1	1000	8	US-11-266-748A-401511	Sequence 401511,
c	40	164.5	5.1	1000	8	US-11-266-748A-472557	Sequence 472557,
	41	164.5	5.1	1097	8	US-11-266-748A-251885	Sequence 251885,
c	42	164.5	5.1	1097	8	US-11-266-748A-312402	Sequence 312402,
	43	155.5	4.8	1025	6	US-10-449-902-10919	Sequence 10919, A
c	44	155	4.8	445	8	US-11-266-748A-177657	Sequence 177657,
	45	148	4.5	861	8	US-11-266-748A-50912	Sequence 50912, A

Search completed: August 5, 2006, 16:32:57

Job time : 289.633 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 5, 2006, 15:42:07 ; Search time 7872.74 Seconds
(without alignments)
6627.009 Million cell updates/sec

Title: US-10-506-624-2
Perfect score: 3257
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 622

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10506624/runat_04082006_171935_9082/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
-USER=US10506624 @CGN_1_1_10834 @runat_04082006_171935_9082 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*

13: gb_gss3:*

14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query		Match Length DB ID				Description
No.	Score	%					
1	2700.5	82.9	4468	6	AK044239		AK044239 Mus muscu
2	1262	38.7	1435	6	AK044368		AK044368 Mus muscu
3	1121.5	34.4	1440	9	DN720019		DN720019 CNB131-D0
4	1057	32.5	648	7	BB278154		BB278154 BB278154
5	1051.5	32.3	1986	14	AY400794		AY400794 Homo sapi
6	1044.5	32.1	1989	14	AY400796		AY400796 Mus muscu
7	1039.5	31.9	3830	6	AK083127		AK083127 Mus muscu
8	955	29.3	751	3	BU209143		BU209143 603102377
9	947	29.1	3300	14	DQ052443		DQ052443 Homo sapi
10	924.5	28.4	1981	14	AY400795		AY400795 Pan trogl
11	919	28.2	4689	6	BC044859		BC044859 Mus muscu
12	915.5	28.1	1671	6	AK089225		AK089225 Mus muscu
13	907	27.8	583	3	BP296424		BP296424 BP296424
14	899	27.6	3300	14	DQ052444		DQ052444 Pan trogl
15	895	27.5	918	10	DV014470		DV014470 CNB286-A1
c 16	887	27.2	772	10	DT313315		DT313315 JGI_CAAX3
17	861.5	26.5	575	9	DA654999		DA654999 DA654999
18	849	26.1	768	5	CJ437585		CJ437585 CJ437585
19	823.5	25.3	903	9	CX566236		CX566236 UI-M-IB0-
20	817	25.1	521	7	BE664838		BE664838 152713 MA
21	816	25.1	567	9	DA239381		DA239381 DA239381
22	798	24.5	725	4	BX865490		BX865490 BX865490
23	796	24.4	967	3	BU139114		BU139114 603134006
24	794	24.4	762	9	CX939714		CX939714 JGI_CAAO6
c 25	791.5	24.3	714	9	CX939713		CX939713 JGI_CAAO6
26	781.5	24.0	1171	9	DN724375		DN724375 CNB18-H02
27	768	23.6	834	9	DN901411		DN901411 naq19e10.
28	766.5	23.5	855	10	DT313316		DT313316 JGI_CAAX3
29	764	23.5	710	2	BG865884		BG865884 602788116
30	763	23.4	670	10	DT317070		DT317070 JGI_CAAX5
31	754.5	23.2	676	2	BJ738554		BJ738554 BJ738554
c 32	750	23.0	660	2	BI878483		BI878483 fl78e05.x
33	747.5	23.0	928	3	BU504837		BU504837 AGENCOURT
34	742	22.8	1113	10	DW618038		DW618038 CLJ302-A1
35	738	22.7	665	8	CN308563		CN308563 170004241
36	738	22.7	668	5	CF733315		CF733315 UI-M-HB0-
37	726.5	22.3	766	10	DT191907		DT191907 JGI_CAAS5
38	718	22.0	424	7	BE653777		BE653777 UI-M-AO1-
39	713	21.9	810	10	DY314335		DY314335 AGENCOURT
40	711	21.8	820	10	DT193060		DT193060 JGI_CAAS1

Search completed: August 5, 2006, 20:34:26
Job time : 7888.74 secs

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OM protein - protein search, using sw model

Run on: August 5, 2006, 11:22:48 ; Search time 133.891 Seconds
(without alignments)
2059.155 Million cell updates/sec

Title: US-10-506-624-4
Perfect score: 3150
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 603

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	ID	Description	
1	3150	100.0	603	5	AAE22088	Aae22088 Human nov	
2	3150	100.0	603	8	ADJ65163	Adj65163 Potassium	
3	3130.5	99.4	622	8	ADJ65161	Adj65161 Potassium	
4	1856	58.9	644	7	ADE31661	Ade31661 Human 692	
5	1856	58.9	704	9	ADX38838	Adx38838 Human can	
6	1856	58.9	709	9	ADX38836	Adx38836 Human can	
7	1846	58.6	353	5	AAE22090	Aae22090 Human nov	

8	1833.5	58.2	593	9	ADX38840	Adx38840	Human	can
9	1811.5	57.5	630	5	ABP69673	Abp69673	Human	pol
10	1735.5	55.1	480	4	ABG12623	Abg12623	Novel	hum
11	1657	52.6	316	5	AAE22089	Aae22089	Human	nov
12	1557	49.4	352	7	ADM04873	Adm04873	Human	pro
13	1557	49.4	352	9	AEC87803	Aec87803	Human	cDN
14	1039	33.0	661	5	ABB84485	Abb84485	Human	NCK
15	1039	33.0	661	6	AAO29752	Aao29752	Human	577
16	1039	33.0	661	7	ADE54756	Ade54756	Human	Pro
17	1039	33.0	661	8	ADH51637	Adh51637	Human	NCK
18	1037	32.9	618	4	AAM78712	Aam78712	Human	pro
19	1031.5	32.7	670	7	ADE54754	Ade54754	Rat	Prote
20	1009.5	32.0	856	4	ABB60425	Abb60425	Drosophil	
21	984.5	31.3	658	4	ABB57820	Abb57820	Drosophil	
22	972.5	30.9	459	9	ADX38839	Adx38839	Human	can
23	959.5	30.5	500	7	ADF69521	Adf69521	Novel	hum
24	954	30.3	1081	7	ADJ68492	Adj68492	Human	hea
25	941	29.9	591	8	ADN23810	Adn23810	Bacterial	
26	941	29.9	591	8	ADN23811	Adn23811	Bacterial	
27	907.5	28.8	235	3	AAB25742	Aab25742	Human	sec
28	875	27.8	611	8	ADN22551	Adn22551	Bacterial	
29	837	26.6	169	3	AAB25701	Aab25701	Human	sec
30	837	26.6	169	6	ADA57589	Ada57589	Human	sec
31	837	26.6	169	6	ADA41486	Ada41486	Human	sec
32	837	26.6	169	6	ABR48142	Abr48142	Human	sec
33	837	26.6	169	6	ABR00299	Abr00299	Human	gen
34	837	26.6	169	7	ADB91829	Adb91829	Human	sec
35	837	26.6	169	7	ADC74600	Adc74600	Human	sec
36	781.5	24.8	481	4	ABB58790	Abb58790	Drosophil	
37	703.5	22.3	168	3	AAB25680	Aab25680	Human	sec
38	703.5	22.3	168	6	ADA57284	Ada57284	Human	sec
39	703.5	22.3	168	6	ADA41165	Ada41165	Human	sec
40	703.5	22.3	168	6	ABR47960	Abr47960	Human	sec
41	703.5	22.3	168	6	ABR00186	Abr00186	Human	gen
42	703.5	22.3	168	7	ADB91690	Adb91690	Human	sec
43	703.5	22.3	168	7	ADC74369	Adc74369	Human	sec
44	693	22.0	168	2	AAY45263	Aay45263	Human	sec
45	693	22.0	168	6	ADA56815	Ada56815	Human	sec

ALIGNMENTS

RESULT 1

AAE22088

ID AAE22088 standard; protein; 603 AA.

XX

AC AAE22088;

XX

DT 25-JUL-2002 (first entry)

XX

DE Human novel ion exchanger protein (NHP) #1.

XX

KW Human; novel ion exchanger protein; NHP; gene mapping; forensic biology;

KW restriction fragment length polymorphism; RFLP analysis; chromosome 14.

XX

OS Homo sapiens.

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XX      WO200226980-A2.
XX
PD      04-APR-2002.
XX
PF      24-SEP-2001; 2001WO-US029828.
XX
PR      27-SEP-2000; 2000US-0235745P.
XX
PA      (LEXI-) LEXICON GENETICS INC.
XX
PI      Friddle CJ,  Gerhardt B;
XX
DR      WPI; 2002-362496/39.
DR      N-PSDB; AAD35144.
XX
PT      New isolated nucleic acid molecule for encoding a novel human ion
PT      exchanger protein.
XX
PS      Claim 1; Page 36-37; 40pp; English.
XX
CC      The invention relates to novel human ion exchanger proteins (NHP) and
CC      their corresponding nucleic acid sequences. The nucleic acid sequence of
CC      the invention is used for encoding a novel human ion exchanger protein,
CC      and is useful for the identification of a protein coding sequence and
CC      mapping a unique gene to a particular chromosome. It may also be used as
CC      additional DNA markers for restriction fragment length polymorphism
CC      (RFLP) analysis, and in forensic biology. The present sequence is human
CC      NHP protein. NHP gene is located on chromosome 14
XX
SQ      Sequence 603 AA;

Query Match          100.0%;  Score 3150;  DB 5;  Length 603;
Best Local Similarity 100.0%;  Pred. No. 3.9e-309;
Matches 603;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Db      1  MALRGTLRPLKVRRRREMLPQQVG FVCAVLALVCCASGLFGSLGHKTASASKRVLPD TWR 60

Qy      61 NRKLMAPVNGTQTAKNCTDPAIHEFPTDLFSNKERQHGA VLLHILGALYMFYALAI V CDD 120
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Qy      121 F FVPSLEKICERLHLS EDVAGATFMAAGSSTPELFASVIGVFITHGDVGVGTIVGSA VFN 180
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Qy      181 ILCIIGVCGLFAGQVVRLTWWAVCRDSVYYTISVIVLIVFIYDEQIVWWEGLVLIILYVF 240
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Qy      241 YILIMKYNVKMQAFFTVKQKSIANGNPVNSELEAVKEKPQYGKNPVVMVDEIMSSSPPKF 300
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Db      241 YILIMKYNVKMQAFFTVKQKSIANGNPVNSELEAVKEKPQYGKNPVVMVDEIMSSSPPKF 300

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Search completed: August 5, 2006, 11:27:47
Job time : 137.891 secs

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OM protein - protein search, using sw model

Run on: August 5, 2006, 11:34:38 ; Search time 35.4416 Seconds
(without alignments)
1489.236 Million cell updates/sec

Title: US-10-506-624-4
Perfect score: 3150
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVTFTVNLPMPREDD 603

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3150	100.0	603	2	US-09-961-679-2 Sequence 2, Appli
2	1846	58.6	353	2	US-09-961-679-6 Sequence 6, Appli
3	1657	52.6	316	2	US-09-961-679-4 Sequence 4, Appli
4	528	16.8	222	2	US-09-270-767-41682 Sequence 41682, A
5	528	16.8	222	2	US-09-270-767-56927 Sequence 56927, A
6	250.5	8.0	539	2	US-09-701-068-2 Sequence 2, Appli
7	233.5	7.4	474	2	US-09-701-068-5 Sequence 5, Appli
8	217.5	6.9	325	2	US-09-489-039A-13618 Sequence 13618, A
9	176	5.6	355	2	US-09-543-681A-5929 Sequence 5929, Ap
10	168	5.3	357	2	US-09-270-767-32690 Sequence 32690, A

11	168	5.3	357	2	US-09-270-767-47907	Sequence 47907, A
12	145	4.6	97	2	US-09-270-767-31865	Sequence 31865, A
13	139	4.4	508	2	US-09-248-796A-20809	Sequence 20809, A
14	135	4.3	333	2	US-09-270-767-32349	Sequence 32349, A
15	135	4.3	333	2	US-09-270-767-47566	Sequence 47566, A
16	125	4.0	168	2	US-09-248-796A-20808	Sequence 20808, A
17	116	3.7	634	2	US-09-949-016-7542	Sequence 7542, Ap
18	115	3.7	555	2	US-10-104-047-3369	Sequence 3369, Ap
19	110.5	3.5	318	2	US-09-270-767-44026	Sequence 44026, A
20	110	3.5	500	2	US-09-489-039A-10995	Sequence 10995, A
21	109.5	3.5	324	2	US-09-605-703B-1356	Sequence 1356, Ap
22	105	3.3	292	2	US-09-543-681A-7272	Sequence 7272, Ap
23	103.5	3.3	403	2	US-09-489-039A-9921	Sequence 9921, Ap
24	103	3.3	197	2	US-09-385-219A-32	Sequence 32, Appl
25	103	3.3	723	2	US-09-248-796A-15245	Sequence 15245, A
26	102.5	3.3	285	2	US-09-248-796A-18821	Sequence 18821, A
27	102	3.2	398	2	US-09-248-796A-20428	Sequence 20428, A
28	101	3.2	486	2	US-09-328-352-6007	Sequence 6007, Ap
29	101	3.2	921	1	US-08-568-459A-8	Sequence 8, Appli
30	101	3.2	921	1	US-08-487-826B-8	Sequence 8, Appli
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32	101	3.2	921	2	US-10-153-273-8	Sequence 8, Appli
33	100.5	3.2	666	2	US-10-104-047-2217	Sequence 2217, Ap
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35	100	3.2	562	2	US-09-328-352-4694	Sequence 4694, Ap
36	99	3.1	695	2	US-10-104-047-2395	Sequence 2395, Ap
37	99	3.1	1444	2	US-09-949-016-9652	Sequence 9652, Ap
38	99	3.1	2004	2	US-09-538-092-1371	Sequence 1371, Ap
39	99	3.1	2004	2	US-09-949-016-6756	Sequence 6756, Ap
40	98.5	3.1	345	2	US-08-718-738-2	Sequence 2, Appli
41	98.5	3.1	345	2	US-09-221-844-2	Sequence 2, Appli
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43	98.5	3.1	351	2	US-09-949-016-8079	Sequence 8079, Ap
44	98.5	3.1	517	2	US-09-815-923-16	Sequence 16, Appl
45	97.5	3.1	634	2	US-09-489-039A-8399	Sequence 8399, Ap

ALIGNMENTS

RESULT 1

US-09-961-679-2

; Sequence 2, Application US/09961679

; Patent No. 6787352

; GENERAL INFORMATION:

; APPLICANT: Friddle, Carl Johan

; APPLICANT: Gerhardt, Brenda

; TITLE OF INVENTION: No. 6787352e1 Human Ion-Exchanger Proteins and Polynucleotides Encoding the

; TITLE OF INVENTION: Same

; FILE REFERENCE: LEX-0239-USA

; CURRENT APPLICATION NUMBER: US/09/961,679

; CURRENT FILING DATE: 2001-09-24

; PRIOR APPLICATION NUMBER: US 60/235,745

; PRIOR FILING DATE: 2000-09-27

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2
 ; LENGTH: 603
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-09-961-679-2

Query Match 100.0%; Score 3150; DB 2; Length 603;
 Best Local Similarity 100.0%; Pred. No. 1.1e-291;
 Matches 603; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    121 FFVPSLEKICERLHLS EDVAGATFMAAGSSTPELFASVIGVFITHGDVGVGTIVGSAVFN 180
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Qy     601 EDD 603
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Db     601 EDD 603

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Search completed: August 5, 2006, 11:36:35
 Job time : 37.4416 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 5, 2006, 11:35:38 ; Search time 123.061 Seconds
(without alignments)
2269.753 Million cell updates/sec

Title: US-10-506-624-4
Perfect score: 3150
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 603

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3150	100.0	603	3	US-09-961-679-2 Sequence 2, Appli
2	3150	100.0	603	5	US-10-886-518-2 Sequence 2, Appli
3	3150	100.0	603	5	US-10-506-624-4 Sequence 4, Appli
4	3130.5	99.4	622	5	US-10-506-624-2 Sequence 2, Appli
5	1856	58.9	644	4	US-10-353-690-18 Sequence 18, Appli
6	1846	58.6	353	3	US-09-961-679-6 Sequence 6, Appli
7	1846	58.6	353	5	US-10-886-518-6 Sequence 6, Appli
8	1735.5	55.1	480	5	US-10-450-763-42982 Sequence 42982, A
9	1657	52.6	316	3	US-09-961-679-4 Sequence 4, Appli
10	1657	52.6	316	5	US-10-886-518-4 Sequence 4, Appli
11	1557	49.4	352	4	US-10-108-260A-3558 Sequence 3558, Ap

12	1039	33.0	661	4	US-10-094-214-5	Sequence 5, Appli
13	1039	33.0	661	4	US-10-281-868-2	Sequence 2, Appli
14	1039	33.0	661	4	US-10-391-399-17	Sequence 17, Appl
15	1009.5	32.0	856	6	US-11-097-143-8067	Sequence 8067, Ap
16	984.5	31.3	658	6	US-11-097-143-252	Sequence 252, App
17	959.5	30.5	500	4	US-10-264-104-2	Sequence 2, Appli
18	954	30.3	1081	4	US-10-408-765A-298	Sequence 298, App
19	941	29.9	591	4	US-10-369-493-6463	Sequence 6463, Ap
20	941	29.9	591	4	US-10-369-493-6464	Sequence 6464, Ap
21	907.5	28.8	235	3	US-09-985-153-133	Sequence 133, App
22	875	27.8	611	4	US-10-369-493-5204	Sequence 5204, Ap
23	837	26.6	169	3	US-09-985-153-90	Sequence 90, Appl
24	837	26.6	169	5	US-10-472-533-588	Sequence 588, App
25	781.5	24.8	481	6	US-11-097-143-3162	Sequence 3162, Ap
26	703.5	22.3	168	3	US-09-985-153-69	Sequence 69, Appl
27	703.5	22.3	168	5	US-10-472-533-475	Sequence 475, App
28	693	22.0	168	3	US-09-798-889-51	Sequence 51, Appl
29	693	22.0	168	4	US-10-633-680-51	Sequence 51, Appl
30	644.5	20.5	353	6	US-11-097-143-1746	Sequence 1746, Ap
31	610	19.4	137	5	US-10-450-763-42981	Sequence 42981, A
32	387.5	12.3	227	4	US-10-264-104-5	Sequence 5, Appli
33	382	12.1	362	6	US-11-097-143-38151	Sequence 38151, A
34	360.5	11.4	584	4	US-10-168-651-5	Sequence 5, Appli
35	355.5	11.3	584	4	US-10-094-214-2	Sequence 2, Appli
36	355.5	11.3	584	4	US-10-391-399-14	Sequence 14, Appl
37	346	11.0	585	6	US-11-012-762-6	Sequence 6, Appli
38	324	10.3	489	4	US-10-437-963-190947	Sequence 190947,
39	322.5	10.2	636	6	US-11-096-568A-12978	Sequence 12978, A
40	322.5	10.2	690	6	US-11-096-568A-12977	Sequence 12977, A
41	307.5	9.8	329	5	US-10-506-454-951	Sequence 951, App
42	304	9.7	559	6	US-11-096-568A-30130	Sequence 30130, A
43	303.5	9.6	494	6	US-11-096-568A-12979	Sequence 12979, A
44	303	9.6	634	4	US-10-425-115-317894	Sequence 317894,
45	300.5	9.5	560	6	US-11-097-143-36060	Sequence 36060, A

Search completed: August 5, 2006, 11:40:51
 Job time : 125.061 secs

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OM protein - protein search, using sw model

Run on: August 5, 2006, 11:36:48 ; Search time 20.6743 Seconds
(without alignments)
1951.660 Million cell updates/sec

Title: US-10-506-624-4
Perfect score: 3150
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 603

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 236815 seqs, 66914042 residues

Total number of hits satisfying chosen parameters: 236815

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1557	49.4	352	7	US-11-293-697-3558 Sequence 3558, Ap
2	322.5	10.2	636	6	US-10-953-349-32706 Sequence 32706, A
3	322.5	10.2	636	7	US-11-056-355B-63281 Sequence 63281, A
4	322.5	10.2	690	6	US-10-953-349-32705 Sequence 32705, A
5	322.5	10.2	690	7	US-11-056-355B-63280 Sequence 63280, A
6	304	9.7	559	7	US-11-056-355B-72751 Sequence 72751, A
7	303.5	9.6	494	6	US-10-953-349-32707 Sequence 32707, A
8	303.5	9.6	494	7	US-11-056-355B-63282 Sequence 63282, A
9	285	9.0	570	6	US-10-953-349-6076 Sequence 6076, Ap

10	285	9.0	570	7	US-11-056-355B-29539	Sequence 29539, A
11	285	9.0	570	7	US-11-056-355B-33129	Sequence 33129, A
12	281.5	8.9	528	7	US-11-056-355B-87545	Sequence 87545, A
13	278	8.8	545	7	US-11-056-355B-81068	Sequence 81068, A
14	278	8.8	580	7	US-11-056-355B-81067	Sequence 81067, A
15	278	8.8	597	6	US-10-449-902-53836	Sequence 53836, A
16	278	8.8	643	7	US-11-056-355B-81066	Sequence 81066, A
17	251	8.0	523	6	US-10-449-902-44629	Sequence 44629, A
18	237.5	7.5	430	6	US-10-953-349-6077	Sequence 6077, Ap
19	237.5	7.5	430	7	US-11-056-355B-29540	Sequence 29540, A
20	237.5	7.5	430	7	US-11-056-355B-33130	Sequence 33130, A
21	205	6.5	406	7	US-11-056-355B-72752	Sequence 72752, A
22	182.5	5.8	375	7	US-11-056-355B-87546	Sequence 87546, A
23	180	5.7	1084	6	US-10-449-902-41128	Sequence 41128, A
24	155	4.9	265	6	US-10-449-902-39371	Sequence 39371, A
25	152.5	4.8	310	6	US-10-953-349-6078	Sequence 6078, Ap
26	152.5	4.8	310	7	US-11-056-355B-29541	Sequence 29541, A
27	152.5	4.8	310	7	US-11-056-355B-33131	Sequence 33131, A
28	105.5	3.3	364	7	US-11-056-355B-20081	Sequence 20081, A
29	105.5	3.3	382	7	US-11-056-355B-20080	Sequence 20080, A
30	105.5	3.3	405	7	US-11-056-355B-20079	Sequence 20079, A
31	105	3.3	2801	6	US-10-540-898-630	Sequence 630, App
32	103	3.3	197	7	US-11-106-014-32	Sequence 32, Appl
33	99	3.1	197	7	US-11-056-355B-64591	Sequence 64591, A
34	98.5	3.1	327	6	US-10-374-780A-178	Sequence 178, App
35	98.5	3.1	345	7	US-11-289-102-322	Sequence 322, App
36	98.5	3.1	497	7	US-11-289-102-312	Sequence 312, App
37	98	3.1	26	7	US-11-134-871-414	Sequence 414, App
38	98	3.1	437	6	US-10-449-902-47968	Sequence 47968, A
39	98	3.1	493	7	US-11-056-355B-43894	Sequence 43894, A
40	98	3.1	493	7	US-11-056-355B-46129	Sequence 46129, A
41	98	3.1	513	7	US-11-056-355B-43893	Sequence 43893, A
42	98	3.1	513	7	US-11-056-355B-46128	Sequence 46128, A
43	98	3.1	585	7	US-11-056-355B-43892	Sequence 43892, A
44	98	3.1	585	7	US-11-056-355B-46127	Sequence 46127, A
45	96.5	3.1	462	6	US-10-471-571A-4604	Sequence 4604, Ap

Search completed: August 5, 2006, 11:41:38

Job time : 22.6743 secs

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OM protein - protein search, using sw model

Run on: August 5, 2006, 11:28:08 ; Search time 26.5812 Seconds
(without alignments)
2182.695 Million cell updates/sec

Title: US-10-506-624-4
Perfect score: 3150
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 603

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	970.5	30.8	1014	2	T31433	Na+/Ca2+, K+-exchan
2	941	29.9	591	2	T19746	hypothetical prote
3	917	29.1	1199	2	S20969	Na+/Ca2+, K+-exchan
4	875	27.8	611	2	T21747	hypothetical prote
5	393	12.5	590	2	S40707	hypothetical prote
6	373.5	11.9	743	2	T38674	probable membrane
7	330	10.5	651	2	T03889	Na+/Ca2+, K+-exchan
8	301.5	9.6	703	2	T03888	Na+/Ca2+, K+-exchan
9	289.5	9.2	644	2	B96582	hypothetical prote
10	286.5	9.1	546	2	D86221	hypothetical prote
11	275.5	8.7	591	2	S40705	Na+/Ca2+, K+-exchan
12	265.5	8.4	807	2	T24110	hypothetical prote
13	264.5	8.4	433	2	S74922	hypothetical prote

14	258	8.2	332	2	H82064	conserved hypothet
15	256	8.1	330	2	H69020	probable Na ⁺ /Ca ²⁺ ,
16	251	8.0	538	2	T00424	probable Na ⁺ /Ca ²⁺
17	244.5	7.8	762	2	S67765	probable membrane
18	236	7.5	302	2	C64311	Na ⁺ /Ca ²⁺ -exchangin
19	231.5	7.3	318	2	A83708	hypothetical prote
20	226	7.2	322	2	E69009	cation antiporter
21	224.5	7.1	324	2	AI0434	probable sodium/ca
22	218.5	6.9	309	2	B72342	conserved hypothet
23	218.5	6.9	890	2	B89047	protein C10G8.5 [i
24	217	6.9	344	2	E84376	Na ⁺ /Ca ²⁺ -exchangin
25	216.5	6.9	325	2	C91138	hypothetical prote
26	216.5	6.9	325	2	F85983	hypothetical prote
27	215.5	6.8	325	2	F65110	hypothetical 34.7
28	211.5	6.7	325	2	AI0904	probable membrane
29	207	6.6	935	2	S43730	Na ⁺ /Ca ²⁺ -exchangin
30	207	6.6	941	2	B53335	Na ⁺ /Ca ²⁺ -exchangin
31	206.5	6.6	921	2	A54139	Na ⁺ /Ca ²⁺ -exchangin
32	202.5	6.4	314	2	C75003	na ⁺ /ca ⁺ exchanging
33	202	6.4	957	2	A53789	Na ⁺ /Ca ²⁺ -exchangin
34	200.5	6.4	958	2	S32435	Na ⁺ /Ca ²⁺ -exchangin
35	195.5	6.2	400	2	T49810	hypothetical prote
36	194.5	6.2	970	2	I48097	Na ⁺ /Ca ²⁺ -exchangin
37	192.5	6.1	325	2	D71159	probable Na ⁺ /Ca ²⁺ -
38	192.5	6.1	973	2	S32815	Na ⁺ /Ca ²⁺ -exchangin
39	190	6.0	971	2	S28833	Na ⁺ /Ca ²⁺ -exchangin
40	189.5	6.0	970	2	A36417	Na ⁺ /Ca ²⁺ -exchangin
41	186.5	5.9	322	2	E70306	conserved hypothet
42	172.5	5.5	160	2	T45258	hypothetical prote
43	172	5.5	970	2	S27114	Na ⁺ /Ca ²⁺ -exchangin
44	169.5	5.4	341	2	A71250	conserved hypothet
45	167	5.3	158	2	S68978	Na ⁺ /Ca ²⁺ , K ⁺ -exchan

Search completed: August 5, 2006, 11:35:19
Job time : 30.5812 secs

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OM protein - protein search, using sw model

Run on: August 5, 2006, 11:23:23 ; Search time 189.514 Seconds
 (without alignments)
 2943.231 Million cell updates/sec

Title: US-10-506-624-4
 Perfect score: 3150
 Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 603

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	3047.5	96.7	605	1 NCKX4_HUMAN	Q8nff2 homo sapien
2	2915.5	92.6	605	1 NCKX4_MOUSE	Q8cgg8 mus musculu
3	1999	63.5	569	2 Q567G1_BRARE	Q567g1 brachydanio
4	1856	58.9	644	2 Q9H417_HUMAN	Q9h417 homo sapien
5	1855	58.9	644	1 NCKX3_HUMAN	Q9hc58 homo sapien
6	1848.5	58.7	645	1 NCKX3_MOUSE	Q99pd7 mus musculu
7	1841	58.4	504	2 Q4RA60_TETNG	Q4ra60 tetraodon n
8	1831	58.1	624	1 NCKX3_RAT	Q9epq0 rattus norv
9	1827	58.0	595	2 Q8VD29_MOUSE	Q8vd29 mus musculu
10	1690	53.7	569	2 Q4S2I3_TETNG	Q4s2i3 tetraodon n
11	1635.5	51.9	588	2 Q4RZL6_TETNG	Q4rzl6 tetraodon n
12	1280.5	40.7	529	2 Q4SFH8_TETNG	Q4sfh8 tetraodon n
13	1173.5	37.3	557	2 Q4RPD9_TETNG	Q4rpd9 tetraodon n
14	1090.5	34.6	538	2 Q7QH05_ANOGA	Q7qh05 anopheles g
15	1085	34.4	536	2 Q5TVP5_ANOGA	Q5tvp5 anopheles g

16	1039	33.0	661	1	NCKX2_HUMAN	Q9ui40	homo sapien
17	1038	33.0	628	2	Q7PQ73_ANOGA	Q7pq73	anopheles g
18	1032	32.8	666	2	Q8BUN9_MOUSE	Q8bun9	mus musculu
19	1031.5	32.7	670	1	NCKX2_RAT	O54701	rattus norv
20	1026	32.6	651	1	NCKX2_CHICK	Q9ial7	gallus gall
21	1024.5	32.5	526	2	Q7PLW1_DROME	Q7plw1	drosophila
22	1024.5	32.5	535	2	Q8SXS9_DROME	Q8sxs9	drosophila
23	1024.5	32.5	542	2	Q5LJX8_DROME	Q5ljx8	drosophila
24	1016.5	32.3	547	2	Q5TQC5_ANOGA	Q5tqc5	anopheles g
25	1016.5	32.3	663	1	NCKX1_CHICK	Q9ial8	gallus gall
26	1013	32.2	576	2	Q7PNG2_ANOGA	Q7png2	anopheles g
27	1009.5	32.0	856	1	NCKX_DROME	Q9u6a0	drosophila
28	1006.5	32.0	888	2	Q8IPE3_DROME	Q8ipe3	drosophila
29	1002.5	31.8	642	2	Q8IPM4_DROME	Q8ipm4	drosophila
30	999	31.7	1043	2	Q4RGI0_TETNG	Q4rgi0	tetraodon n
31	986.5	31.3	513	1	NCKX5_BRARE	Q49sh1	brachydanio
32	974.5	30.9	596	2	Q7PSK6_ANOGA	Q7psk6	anopheles g
33	970.5	30.8	1014	2	O62805_TURTR	O62805	tursiops tr
34	959.5	30.5	500	1	NCKX5_HUMAN	Q7lrs6	homo sapien
35	953	30.3	585	2	Q61JX9_CAEBR	Q61jx9	caenorhabdi
36	952	30.2	1099	1	NCKX1_HUMAN	O60721	homo sapien
37	941	29.9	591	2	O62088_CAEEL	O62088	caenorhabdi
38	931	29.6	487	2	Q4SHN8_TETNG	Q4shn8	tetraodon n
39	925	29.4	1130	2	Q91WD8_MOUSE	Q91wd8	mus musculu
40	919	29.2	501	1	NCKX5_MOUSE	Q8c261	mus musculu
41	915	29.0	647	2	Q4SLY4_TETNG	Q4sly4	tetraodon n
42	908.5	28.8	1216	1	NCKX1_BOVIN	Q28139	bos taurus
43	890.5	28.3	596	2	Q61XS1_CAEBR	Q61xs1	caenorhabdi
44	885.5	28.1	1181	1	NCKX1_RAT	Q9qzm6	rattus norv
45	881	28.0	596	2	O62306_CAEEL	O62306	caenorhabdi

Search completed: August 5, 2006, 11:34:18

Job time : 192.514 secs

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 5, 2006, 15:09:07 ; Search time 991.381 Seconds
(without alignments)
6361.225 Million cell updates/sec

Title: US-10-506-624-4
Perfect score: 3150
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 603

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB spool/US10506624/runat_04082006_171931_9028/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000000 -HOST=abss08
-USER=US10506624_@CGN_1_1_1350_@runat_04082006_171931_9028 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq 8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

14: geneseqn2005s:*

15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3150	100.0	1812	6	AAD35144	Aad35144 Human nov
2	3150	100.0	1845	12	ADJ65162	Adj65162 Potassium
3	3150	100.0	2366	6	AAD35147	Aad35147 Human nov
4	3130.5	99.4	1902	12	ADJ65160	Adj65160 Potassium
5	1856	58.9	3763	10	ADE31660	Ade31660 Human 692
6	1856	58.9	3874	14	ADX38783	Adx38783 Human can
7	1856	58.9	3889	14	ADX38781	Adx38781 Human can
8	1856	58.9	3919	14	ADX38784	Adx38784 Human can
9	1855	58.9	3828	14	ADX38670	Adx38670 Human can
10	1846	58.6	1062	6	AAD35146	Aad35146 Human nov
11	1833.5	58.2	3577	14	ADX38588	Adx38588 Human can
12	1833.5	58.2	3577	14	ADX38675	Adx38675 Human can
13	1811.5	57.5	2036	6	ABZ11890	Abz11890 Human pol
14	1811.5	57.5	2036	12	ADM44408	Adm44408 Novel hum
15	1735.5	55.1	1443	5	AAS76810	Aas76810 DNA encod
16	1706	54.2	2296	11	ADM02430	Adm02430 Human cDN
17	1706	54.2	2296	14	AEC85360	Aec85360 Human cDN
18	1657	52.6	951	6	AAD35145	Aad35145 Human nov
19	1046.5	33.2	2194	3	AAA87702	Aaa87702 Human sec
20	1046.5	33.2	2194	8	ADA40550	Ada40550 Human sec
21	1046.5	33.2	2194	8	ACC50853	Acc50853 Human sec
22	1046.5	33.2	2194	8	ABZ71478	Abz71478 Secreted
23	1046.5	33.2	2194	9	ADB91445	Adb91445 Human sec
24	1046.5	33.2	2194	10	ADC73985	Adc73985 Human sec
25	1046.5	33.2	2194	10	ADA56696	Ada56696 Gene enco
26	1039	33.0	2221	8	AAL60325	Aal60325 Human 577
27	1039	33.0	2221	14	ADZ49507	Adz49507 Insulin s
28	1039	33.0	2513	4	AAK51845	Aak51845 Human pol
29	1009.5	32.0	3308	3	AAA87681	Aaa87681 Human sec
30	1009.5	32.0	3308	8	ADA40228	Ada40228 Human sec
31	1009.5	32.0	3308	8	ACC50671	Acc50671 Human sec
32	1009.5	32.0	3308	8	ABZ71365	Abz71365 Secreted
33	1009.5	32.0	3308	9	ADB91306	Adb91306 Human sec
34	1009.5	32.0	3308	10	ADC73754	Adc73754 Human sec
35	1009.5	32.0	3308	10	ADA56388	Ada56388 Gene enco
36	1009.5	32.0	3575	4	ABL07217	Abl07217 Drosophila
37	1009	32.0	3306	3	AAA87701	Aaa87701 Human sec
38	1009	32.0	3306	8	ADA40549	Ada40549 Human sec
39	1009	32.0	3306	8	ACC50852	Acc50852 Human sec
40	1009	32.0	3306	8	ABZ71477	Abz71477 Secreted
41	1009	32.0	3306	9	ADB91444	Adb91444 Human sec
42	1009	32.0	3306	10	ADC73984	Adc73984 Human sec
43	1009	32.0	3306	10	ADA56695	Ada56695 Gene enco
44	1000	31.7	1683	4	ABL03947	Abl03947 Drosophila
45	986	31.3	2359	4	ABL02007	Abl02007 Drosophila

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 5, 2006, 15:51:16 ; Search time 1877.91 Seconds
 (without alignments)
 5918.356 Million cell updates/sec

Title: US-10-506-624-4
 Perfect score: 3150
 Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 603

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
 -Q=/abss/ABSSWEB_spool/US10506624/runat_04082006_171939_9185/app_query.fasta_1
 -DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
 -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
 -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000000 -HOST=abss07
 -USER=US10506624_@CGN_1_1_2380_@runat_04082006_171939_9185 -NCPU=6 -ICPU=3
 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3150	100.0	1812	3	US-09-961-679-1	Sequence 1, Appli
2	3150	100.0	1812	10	US-10-886-518-1	Sequence 1, Appli
3	3150	100.0	1845	10	US-10-506-624-3	Sequence 3, Appli
4	3150	100.0	2366	3	US-09-961-679-7	Sequence 7, Appli
5	3150	100.0	2366	10	US-10-886-518-7	Sequence 7, Appli
6	3130.5	99.4	1902	10	US-10-506-624-1	Sequence 1, Appli
7	1856	58.9	3763	7	US-10-353-690-17	Sequence 17, Appl
8	1846	58.6	1062	3	US-09-961-679-5	Sequence 5, Appli
9	1846	58.6	1062	10	US-10-886-518-5	Sequence 5, Appli
10	1811.5	57.5	2036	8	US-10-302-172-772	Sequence 772, App
11	1735.5	55.1	1443	10	US-10-450-763-12614	Sequence 12614, A
12	1706	54.2	2296	7	US-10-108-260A-1115	Sequence 1115, Ap
13	1657	52.6	951	3	US-09-961-679-3	Sequence 3, Appli
14	1657	52.6	951	10	US-10-886-518-3	Sequence 3, Appli
15	1046.5	33.2	2194	3	US-09-985-153-47	Sequence 47, Appl
16	1046.5	33.2	2194	10	US-10-472-533-299	Sequence 299, App
17	1039	33.0	600	13	US-11-060-756-4124	Sequence 4124, Ap
18	1039	33.0	600	13	US-11-060-756-8396	Sequence 8396, Ap
19	1039	33.0	2221	7	US-10-281-868-1	Sequence 1, Appli
20	1039	33.0	2221	7	US-10-281-868-3	Sequence 3, Appli
21	1039	33.0	2221	10	US-10-887-553A-836	Sequence 836, App
22	1009.5	32.0	3308	3	US-09-985-153-26	Sequence 26, Appl
23	1009.5	32.0	3308	10	US-10-472-533-186	Sequence 186, App
24	1009.5	32.0	3575	13	US-11-097-143-8066	Sequence 8066, Ap
25	1009	32.0	3306	3	US-09-985-153-46	Sequence 46, Appl
26	1009	32.0	3306	10	US-10-472-533-298	Sequence 298, App
27	1000	31.7	1683	13	US-11-097-143-3161	Sequence 3161, Ap
28	986	31.3	2359	13	US-11-097-143-251	Sequence 251, App
29	959.5	30.5	1503	6	US-10-264-104-3	Sequence 3, Appli
30	959.5	30.5	1596	6	US-10-264-104-1	Sequence 1, Appli
31	885.5	28.1	3897	16	US-11-136-527-2555	Sequence 2555, Ap
32	851	27.0	2492	3	US-09-798-889-43	Sequence 43, Appl
33	851	27.0	2492	8	US-10-633-680-43	Sequence 43, Appl
34	848	26.9	1489	3	US-09-798-889-17	Sequence 17, Appl
35	848	26.9	1489	8	US-10-633-680-17	Sequence 17, Appl
c 36	846.5	26.9	7993	13	US-11-097-143-250	Sequence 250, App
37	682	21.7	12663	13	US-11-097-143-3160	Sequence 3160, Ap
38	648.5	20.6	1094	13	US-11-097-143-1745	Sequence 1745, Ap
39	610	19.4	415	10	US-10-450-763-12613	Sequence 12613, A

Search completed: August 5, 2006, 20:02:35
 Job time : 1893.91 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 5, 2006, 15:45:16 ; Search time 274.673 Seconds
 (without alignments)
 6161.581 Million cell updates/sec

Title: US-10-506-624-4
 Perfect score: 3150
 Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 603

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
 -Q=/abss/ABSSWEB_spool/US10506624/runat_04082006_171937_9122/app_query.fasta_1
 -DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
 -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -HOST=abss03p -USER=US10506624_@CGN_1_1_381_@runat_04082006_171937_9122
 -NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	3150	100.0	1812	3	US-09-961-679-1	Sequence 1, Appli
	2	3150	100.0	2366	3	US-09-961-679-7	Sequence 7, Appli
	3	1846	58.6	1062	3	US-09-961-679-5	Sequence 5, Appli
	4	1811.5	57.5	2036	3	US-09-799-451-772	Sequence 772, App
	5	1657	52.6	951	3	US-09-961-679-3	Sequence 3, Appli
	6	528	16.8	1174	3	US-09-270-767-25428	Sequence 25428, A
	7	528	16.8	1612	3	US-09-270-767-10086	Sequence 10086, A
	8	493	15.7	744	3	US-09-976-594-1120	Sequence 1120, Ap
	9	328	10.4	2412	3	US-09-799-451-229	Sequence 229, App
	10	256	8.1	1935	3	US-09-701-068-3	Sequence 3, Appli
	11	256	8.1	1950	3	US-09-701-068-1	Sequence 1, Appli
c	12	236	7.5	1664976	3	US-08-916-421B-1	Sequence 1, Appli
c	13	236	7.5	1664976	3	US-09-692-570-1	Sequence 1, Appli
	14	231.5	7.3	3431	3	US-09-221-017B-993	Sequence 993, App
	15	221.5	7.0	546	3	US-09-702-705-129	Sequence 129, App
	16	221.5	7.0	546	3	US-09-736-457-129	Sequence 129, App
	17	221.5	7.0	546	3	US-09-614-124B-129	Sequence 129, App
	18	221.5	7.0	546	3	US-09-671-325-129	Sequence 129, App
	19	221.5	7.0	546	3	US-09-589-184-129	Sequence 129, App
	20	221.5	7.0	546	3	US-09-658-824-129	Sequence 129, App
	21	221.5	7.0	546	3	US-10-017-754-129	Sequence 129, App
	22	221.5	7.0	546	3	US-09-651-563-129	Sequence 129, App
	23	221.5	7.0	546	3	US-09-519-642-129	Sequence 129, App
	24	217.5	6.9	978	3	US-09-489-039A-6447	Sequence 6447, Ap
	25	180.5	5.7	1071	3	US-09-270-767-1061	Sequence 1061, Ap
	26	180.5	5.7	1071	3	US-09-270-767-16343	Sequence 16343, A
	27	176	5.6	1068	3	US-09-543-681A-1757	Sequence 1757, Ap
	28	163	5.2	999	3	US-09-270-767-720	Sequence 720, App
	29	163	5.2	999	3	US-09-270-767-16002	Sequence 16002, A
c	30	145	4.6	964	3	US-09-270-767-236	Sequence 236, App
c	31	145	4.6	964	3	US-09-270-767-15518	Sequence 15518, A
c	32	145	4.6	1684	3	US-10-104-047-1419	Sequence 1419, Ap
	33	143.5	4.6	2803	3	US-09-701-068-4	Sequence 4, Appli
	34	142.5	4.5	1527	3	US-09-248-796A-6706	Sequence 6706, Ap
c	35	126	4.0	592	3	US-09-669-751-77	Sequence 77, Appl
	36	125	4.0	507	3	US-09-248-796A-6705	Sequence 6705, Ap
	37	124	3.9	52655	3	US-09-949-016-13495	Sequence 13495, A
c	38	119.5	3.8	1987	3	US-09-949-016-1536	Sequence 1536, Ap
	39	116	3.7	4371	3	US-09-949-016-1671	Sequence 1671, Ap
	40	115	3.7	2062	3	US-10-104-047-1399	Sequence 1399, Ap
c	41	114.5	3.6	1864	2	US-08-454-720A-38	Sequence 38, Appl
	42	111	3.5	1299	3	US-09-603-208A-133	Sequence 133, App
	43	110.5	3.5	954	3	US-09-270-767-12445	Sequence 12445, A
	44	110	3.5	1503	3	US-09-489-039A-3824	Sequence 3824, Ap
	45	110	3.5	3213	3	US-09-949-016-2951	Sequence 2951, Ap

Search completed: August 5, 2006, 20:42:18
Job time : 1449.67 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 5, 2006, 16:10:57 ; Search time 262.367 Seconds
 (without alignments)
 5460.220 Million cell updates/sec

Title: US-10-506-624-4
 Perfect score: 3150
 Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMPREDD 603

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 2193277 seqs, 791917567 residues

Total number of hits satisfying chosen parameters: 4386554

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
 -Q=/abss/ABSSWEB_spool/US10506624/runat_04082006_171941_9232/app_query.fasta_1
 -DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptp -NORM=ext -HEAPSIZE=500 -MINLEN=0
 -MAXLEN=2000000000 -HOST=abss04
 -USER=US10506624 @CGN_1_1_306 @runat_04082006_171941_9232 -NCPU=6 -ICPU=3
 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	1706	54.2	2296	8	US-11-293-697-1115	Sequence 1115, Ap
	2	959.5	30.5	1617	8	US-11-266-748A-23635	Sequence 23635, A
	3	959.5	30.5	1617	8	US-11-266-748A-31757	Sequence 31757, A
c	4	551	17.5	554	8	US-11-266-748A-354597	Sequence 354597,
	5	551	17.5	554	8	US-11-266-748A-437976	Sequence 437976,
	6	484.5	15.4	1000	8	US-11-266-748A-401181	Sequence 401181,
c	7	484.5	15.4	1000	8	US-11-266-748A-472227	Sequence 472227,
	8	369.5	11.7	2993	8	US-11-266-748A-30769	Sequence 30769, A
	9	322.5	10.2	2140	6	US-10-953-349-32704	Sequence 32704, A
	10	322.5	10.2	2140	7	US-11-056-355B-63279	Sequence 63279, A
c	11	313.5	10.0	1670	8	US-11-266-748A-188993	Sequence 188993,
	12	313.5	10.0	1670	8	US-11-266-748A-242690	Sequence 242690,
	13	311	9.9	3033	7	US-11-218-305-12786	Sequence 12786, A
	14	307.5	9.8	1896	6	US-10-449-902-25496	Sequence 25496, A
	15	304	9.7	1680	7	US-11-056-355B-72750	Sequence 72750, A
	16	285	9.0	1871	6	US-10-953-349-6075	Sequence 6075, Ap
	17	285	9.0	1871	7	US-11-056-355B-29538	Sequence 29538, A
	18	285	9.0	1871	7	US-11-056-355B-33128	Sequence 33128, A
	19	281.5	8.9	1587	7	US-11-056-355B-87544	Sequence 87544, A
	20	278	8.8	1932	7	US-11-056-355B-81065	Sequence 81065, A
	21	262.5	8.3	1969	6	US-10-449-902-16206	Sequence 16206, A
	22	246	7.8	2295	8	US-11-217-529-2812	Sequence 2812, Ap
	23	221.5	7.0	546	8	US-11-301-554-129	Sequence 129, App
	24	221.5	7.0	680	8	US-11-266-748A-212830	Sequence 212830,
c	25	221.5	7.0	680	8	US-11-266-748A-236131	Sequence 236131,
	26	217.5	6.9	735	8	US-11-266-748A-255563	Sequence 255563,
c	27	217.5	6.9	735	8	US-11-266-748A-316080	Sequence 316080,
	28	217.5	6.9	1507	8	US-11-266-748A-81568	Sequence 81568, A
c	29	217.5	6.9	1507	8	US-11-266-748A-134379	Sequence 134379,
c	30	207	6.6	3632	7	US-11-218-305-21414	Sequence 21414, A
	31	188	6.0	4282	8	US-11-266-748A-56894	Sequence 56894, A
	32	180.5	5.7	3646	6	US-10-449-902-12682	Sequence 12682, A
c	33	171	5.4	1109	8	US-11-266-748A-355575	Sequence 355575,
	34	171	5.4	1109	8	US-11-266-748A-438954	Sequence 438954,
	35	171	5.4	1436	8	US-11-266-748A-76380	Sequence 76380, A
c	36	171	5.4	1436	8	US-11-266-748A-129191	Sequence 129191,
	37	168	5.3	2172	8	US-11-217-529-3060	Sequence 3060, Ap
	38	164.5	5.2	1000	8	US-11-266-748A-223147	Sequence 223147,
	39	164.5	5.2	1000	8	US-11-266-748A-401511	Sequence 401511,
c	40	164.5	5.2	1000	8	US-11-266-748A-472557	Sequence 472557,
	41	164.5	5.2	1097	8	US-11-266-748A-251885	Sequence 251885,
c	42	164.5	5.2	1097	8	US-11-266-748A-312402	Sequence 312402,
	43	158	5.0	1025	6	US-10-449-902-10919	Sequence 10919, A
c	44	155	4.9	445	8	US-11-266-748A-177657	Sequence 177657,
	45	153.5	4.9	861	8	US-11-266-748A-50912	Sequence 50912, A

Search completed: August 5, 2006, 16:32:38

Job time : 281.367 secs

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 5, 2006, 15:42:07 ; Search time 7632.26 Seconds
(without alignments)
6627.009 Million cell updates/sec

Title: US-10-506-624-4
Perfect score: 3150
Sequence: 1 MALRGTLRPLKVRRRREMLP.....IMIEFNVFTFVNLPMCREDD 603

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
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-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-USER=US10506624 @CGN_1_1_10834 @runat_04082006_171935_9082 -NCPU=6 -ICPU=3
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12: gb_gss2:*

13: gb_gss3:*

14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					Description
	No.	Score	Match	Length	ID	
	1	2718	86.3	4468	6	AK044239 Mus muscu
	2	1262	40.1	1435	6	AK044368 Mus muscu
	3	1121.5	35.6	1440	9	DN720019 CNB131-D0
	4	1057	33.6	648	7	BB278154 BB278154
	5	1039	33.0	1986	14	AY400794 Homo sapi
	6	1037	32.9	1989	14	AY400796 Mus muscu
	7	1032	32.8	3830	6	AK083127 Mus muscu
	8	952	30.2	3300	14	DQ052443 Homo sapi
	9	941	29.9	751	3	BU209143 603102377
	10	919	29.2	1671	6	AK089225 Mus muscu
	11	916	29.1	4689	6	BC044859 Mus muscu
	12	913	29.0	1981	14	AY400795 Pan trogl
	13	907	28.8	583	3	BP296424 BP296424
	14	905.5	28.7	3300	14	DQ052444 Pan trogl
	15	895	28.4	918	10	DV014470 CNB286-A1
c	16	887	28.2	772	10	DT313315 JGI_CAAX3
	17	849	27.0	768	5	CJ437585 CJ437585
	18	821	26.1	903	9	CX566236 UI-M-IB0-
	19	817	25.9	521	7	BE664838 152713 MA
	20	816	25.9	567	9	DA239381 DA239381
	21	815.5	25.9	725	4	BX865490 BX865490
	22	796	25.3	967	3	BU139114 603134006
	23	794	25.2	762	9	CX939714 JGI_CAAO6
c	24	791.5	25.1	714	9	CX939713 JGI_CAAO6
	25	789	25.0	1171	9	DN724375 CNB18-H02
	26	780.5	24.8	670	10	DT317070 JGI_CAAX5
	27	768	24.4	834	9	DN901411 naq19e10.
	28	766.5	24.3	855	10	DT313316 JGI_CAAX3
	29	764	24.3	710	2	BG865884 602788116
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c	32	750	23.8	660	2	BI878483 fl78e05.x
	33	747.5	23.7	928	3	BU504837 AGENCOURT
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	43	700.5	22.2	766	10	DT182244 JGI_ANNO4
c	44	686.5	21.8	452	8	CO994906 UMC-pd12_
	45	686	21.8	581	4	CB592746 AGENCOURT

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 5, 2006, 15:40:21 ; Search time 7949.26 Seconds
(without alignments)
7276.202 Million cell updates/sec

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Perfect score: 3150
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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10: gb_vi:*
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12: gb_htg:*

13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	3150	100.0	2366	2	AX406631	AX406631 Sequence
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8	2949.5	93.6	2094	6	AY156046	AY156046 Mus muscu
9	2918.5	92.7	4419	5	AF520706	AF520706 Homo sapi
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11	2030	64.4	2178	11	BC093185	BC093185 Danio rer
12	1856	58.9	3763	2	DD200094	DD200094 Methods a
13	1855	58.9	3905	5	AF288087	AF288087 Homo sapi
14	1846	58.6	1062	2	AR580278	AR580278 Sequence
15	1846	58.6	1062	2	AX406629	AX406629 Sequence
16	1841	58.4	3637	5	AF169257	AF169257 Homo sapi
17	1833.5	58.2	2392	6	AF314821	AF314821 Mus muscu
18	1831	58.1	1937	6	AY009158	AY009158 Rattus no
19	1827	58.0	3436	6	BC017615	BC017615 Mus muscu
20	1811.5	57.5	2036	2	AR578596	AR578596 Sequence
21	1727	54.8	4766	5	HSM805663	AL834225 Homo sapi
22	1706	54.2	2296	2	CS167870	CS167870 Sequence
23	1706	54.2	2296	2	AX833991	AX833991 Sequence
24	1706	54.2	2296	5	AK096171	AK096171 Homo sapi
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27	1552.5	49.3	1041	2	CQ719073	CQ719073 Sequence
28	1184.5	37.6	955	11	CR386930	CR386930 Gallus ga
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32	1039	33.0	2221	5	AF097366	AF097366 Homo sapi
33	1037	32.9	2016	13	AY084156	AY084156 Drosophil
34	1031.5	32.7	8942	6	AF021923	AF021923 Rattus no
35	1030.5	32.7	2182	11	AF177986	AF177986 Gallus ga
36	1030	32.7	2259	11	AF177984	AF177984 Gallus ga
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45 986.5 31.3 2003 11 AY682553

AY682553 Danio rer

ALIGNMENTS

RESULT 1

AR580276

LOCUS AR580276 1812 bp DNA linear PAT 15-DEC-2004

DEFINITION Sequence 1 from patent US 6787352.

ACCESSION AR580276

VERSION AR580276.1 GI:56610392

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1812)

AUTHORS Friddle,C.J. and Gerhardt,B.

TITLE Polynucleotides encoding human ion-exchanger proteins

JOURNAL Patent: US 6787352-A 1 07-SEP-2004;

Lexicon Genetics Incorporated; The Woodlands, TX

FEATURES Location/Qualifiers

source 1..1812

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.:	0	Length:	1812
Score:	3150.00	Matches:	603
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-506-624-4 (1-603) x AR580276 (1-1812)

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Db	1	ATGGCGCTCCGCGGGACCCCTCCGCGCGCTCAAAGTTCGCAGGAGGCGAGAGATGCTGCCG	60
Qy	21	GlnGlnValGlyPheValCysAlaValLeuAlaLeuValCysCysAlaSerGlyLeuPhe	40
Db	61	CAGCAAGTCGGCTTCGTGTGCGCGGTGCTGGCCCTGGTGTGCTGTGCGTCCGGCCTCTTC	120
Qy	41	GlySerLeuGlyHisLysThrAlaSerAlaSerLysArgValLeuProAspThrTrpArg	60
Db	121	GGCAGCTTGGGGCACAAAACAGCTTCTGCTAGCAAACGTGTCCTGCCAGACACATGGAGA	180
Qy	61	AsnArgLysLeuMetAlaProValAsnGlyThrGlnThrAlaLysAsnCysThrAspPro	80
Db	181	AATAGAAAGTTGATGGCCCCAGTGAATGGGACACAGACAGCCAAGAACTGCACAGATCCT	240
Qy	81	AlaIleHisGluPheProThrAspLeuPheSerAsnLysGluArgGlnHisGlyAlaVal	100
Db	241	GCGATTACAGAGTTCCCCACAGATCTGTTCTCCAATAAGGAGCGACAGCACGGAGCCGTC	300
Qy	101	LeuLeuHisIleLeuGlyAlaLeuTyrMetPheTyrAlaLeuAlaIleValCysAspAsp	120

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Qy      161 ValPheIleThrHisGlyAspValGlyValGlyThrIleValGlySerAlaValPheAsn 180
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Db      481 GTGTTTCATCACCAYGGGGACGTCGGGGTGGGCACCATCGTGGGCTCTGCTGTGTTCAAC 540
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Qy      281 TyrGlyLysAsnProValValMetValAspGluIleMetSerSerSerProProLysPhe 300
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Db      841 TATGGCAAGAACCCCGTGGTGATGGTGGACGAGATTATGAGCTCCAGCCCTCCCAAGTTC 900
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Qy      301 ThrPheProGluAlaGlyLeuArgIleMetIleThrAsnLysPheGlyProArgThrArg 320
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Qy      341 GlyValSerSerLysProLeuGlnAsnGlyArgHisGluAsnIleGluAsnGlyAsnVal 360
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Db      1021 GGTGTGAGCAGTAAGCCGCTTCAAACGGGAGGCACGAGAACATTGAGAACGGGAATGTT 1080
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Qy      361 ProValGluAsnProGluAspProGlnGlnAsnGlnGluGlnGlnProProProGlnPro 380
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Qy      381 ProProProGluProGluProValGluAlaAspPheLeuSerProPheSerValProGlu 400
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Db      1201 GCCAGAGGGGACAAGGTCAAGTGGGTGTTACCTGGCCCCCTCATCTTCTCCTGTGCGTC 1260
Qy      421 ThrIleProAsnCysSerLysProArgTrpGluLysPhePheMetValThrPheIleThr 440
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Db      1261 ACCATTCCCAACTGCAGCAAGCCCCGCTGGGAGAAGTTCTTCATGGTCACCTTCATCACC 1320
Qy      441 AlaThrLeuTrpIleAlaValPheSerTyrIleMetValTrpLeuValThrIleIleGly 460
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Qy      461 TyrThrLeuGlyIleProAspValIleMetGlyIleThrPheLeuAlaAlaGlyThrSer 480
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Qy      521 LeuGlnThrMetValValAsnTyrGlySerThrValLysIleAsnSerArgGlyLeuVal 540
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Qy      581 CysPheSerIleMetIleGluPheAsnValPheThrPheValAsnLeuProMetCysArg 600
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RESULT 2

AX406625

LOCUS AX406625 1812 bp DNA linear PAT 14-JUN-2002

DEFINITION Sequence 1 from Patent WO0226980.

ACCESSION AX406625

VERSION AX406625.1 GI:21439618

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

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Db	541	ATCCTGTGCATAATTGGAGTGTGCGGACTGTTTGCTGGCCAGGTGGTCCGTCTGACGTGG	600
Qy	201	TrpAlaValCysArgAspSerValTyrTyrThrIleSerValIleValLeuIleValPhe	220
Db	601	TGGGCCGTGTGCCGAGACTCCGTGTACTACACCATCTCTGTTCATCGTCTCATCGTGTC	660
Qy	221	IleTyrAspGluGlnIleValTrpTrpGluGlyLeuValLeuIleIleLeuTyrValPhe	240
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Db	721	TATATTCTGATCATGAAGTACAATGTGAAGATGCAAGCCTTTTTCACAGTCAAACAAAAG	780
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Db	1261	ACCATTCCCAACTGCAGCAAGCCCCGCTGGGAGAAGTTCTTCATGGTCACCTTCATCACC	1320
Qy	441	AlaThrLeuTrpIleAlaValPheSerTyrIleMetValTrpLeuValThrIleIleGly	460
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Qy      541 TyrSerValValLeuLeuLeuGlySerValAlaLeuThrValLeuGlyIleHisLeuAsn 560
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Qy      561 LysTrpArgLeuAspArgLysLeuGlyValTyrValLeuValLeuTyrAlaIlePheLeu 580
      |||
Db      1681 AAGTGGCGACTGGACCGGAAGCTGGGTGTCTACGTGCTGGTTCCTACGCCATCTTCTTG 1740

Qy      581 CysPheSerIleMetIleGluPheAsnValPheThrPheValAsnLeuProMetCysArg 600
      |||
Db      1741 TGCTTCTCCATAATGATAGAGTTTAACGTCTTTACCTTCGTCAACTTGCCGATGTGCCGG 1800

Qy      601 GluAspAsp 603
      |||
Db      1801 GAAGACGAT 1809
```

Search completed: August 5, 2006, 20:13:58

Job time : 7994.26 secs